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Legal Date: 03-05-2003

No.	Doccode	Number of pages
1	SRNT	110

Total number of pages: 110

Remarks:

Order of re-scan issued on





A DOCPHOENIX

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CLM _____
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COMPUTER _____
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NPL _____
 Non-Patent Literature
OATH _____
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PET. _____
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SEQLIST _____
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SPEC _____
 Specification
SPEC NO _____
 Specification Not in English
TRNA _____
 Transmittal New Application

CTNF _____
 Count Non-Final
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 Count Restriction
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M903 _____
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M905 _____
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INCOMING

AP.B _____
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Internal

03-05-03 SRNT 100
 Examiner Search Notes
CLMPTO _____
 PTO Prepared Complete Claim Set

ECBOX _____
 Evidence Copy Box Identification
WCLM _____
 Claim Worksheet
WFEE _____
 Fee Worksheet

File Wrapper

FWCLM _____
 File Wrapper Claim
IIFW _____
 File Wrapper Issue Information
SRFW _____
 File Wrapper Search Info

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SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) _____	STN _____
Searcher Phone # _____	AA Sequence (#) _____	Dialog _____
Searcher Location _____	Structure (#) _____	Questel Orbit _____
Date Searcher Picked Up _____	Bibliographic _____	Dr Link _____
Date Completed _____	Litigation _____	Lexis Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems _____
clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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GenCore version 5.1.3
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10M protein - protein search, using sw model

Run on: March 5, 2003, 08:10: Search time 46 seconds
(without alignments)
8,360 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequences: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10 0 0 Gapext 0 5

Searched: 283224 seqs, 96134420 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: PIR 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	20	100.0	28	A27261	proteinase inhibitor
2	20	100.0	37	G28027	protein p10 - curl
3	20	100.0	58	G03810	psl protein - Rhi
4	20	100.0	59	R60212	T-cell surface gly
5	20	100.0	59	AC1286	LSU ribosomal prot
6	20	100.0	61	T03065	cytochrome c oxida
7	20	100.0	62	G00471	hypothetical prote
8	20	100.0	63	P89902	hypothetical prote
9	20	100.0	64	G44484	hypothetical prote
10	20	100.0	77	G73268	hypothetical prote
11	20	100.0	80	T15296	hypothetical prote
12	20	100.0	81	G00154	hypothetical prote
13	20	100.0	92	T42093	hypothetical prote
14	20	100.0	93	T19717	hypothetical prote
15	20	100.0	86	G69107	hypothetical prote
16	20	100.0	89	G73296	hypothetical prote
17	20	100.0	92	TN0349	plastoquinol-plast
18	20	100.0	93	B86755	prophage p12 prote
19	20	100.0	93	A80923	peptidyl-prolyl ci
20	20	100.0	93	F91217	peptidylprolyl iso
21	20	100.0	93	F86063	peptidylprolyl iso
22	20	100.0	93	S48658	peptidylprolyl iso
23	20	100.0	99	T37093	hypothetical prote
24	20	100.0	101	T25656	hypothetical prote
25	20	100.0	102	G22711	probable neurogep
26	20	100.0	103	F86564	Yidd family [impor
27	20	100.0	103	H72060	yidd family Chla
28	20	100.0	104	P4WKEP	ribosomal protein
29	20	100.0	105	S04150	plastoquinol-plast

30	20	100.0	105	2	AE1848	hypothetical prote
31	20	100.0	105	2	S76770	hypothetical prote
32	20	100.0	106	2	F81506	hypothetical prote
33	20	100.0	108	2	T13133	protein p14 - pla
34	20	100.0	108	2	T41447	very hypothetical
35	20	100.0	109	2	F70627	hypothetical prote
36	20	100.0	111	2	D72112	hypothetical prote
37	20	100.0	111	2	F85511	hypothetical prote
38	20	100.0	112	2	B69438	hypothetical prote
39	20	100.0	113	2	T30436	hypothetical prote
40	20	100.0	113	2	F90319	hypothetical prote
41	20	100.0	114	2	H87113	nitrogen regulator
42	20	100.0	115	2	F72716	hypothetical prote
43	20	100.0	115	2	G83426	hypothetical prote
44	20	100.0	116	1	Q0PSHT	hypothetical prote
45	20	100.0	116	1	Q0E8HT	hypothetical prote
46	20	100.0	116	2	G00573	merit protein, 12
47	20	100.0	116	2	B33858	merit protein - Eac
48	20	100.0	116	2	S70142	merit protein - Eac
49	20	100.0	116	2	H96643	hypothetical prote
50	20	100.0	117	2	L69335	serine-threonine dehydrat

ALIGNMENTS

RESULT 1

A27261

proteinase inhibitor 3 - sea anemone (Stichodactyla sp.) (fragments)

C.Species: Stichodactyla sp., Stichodactyla sp.

C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1993

C.Accession: A27261

R.Mebs, D.; Gebauer, E.

Toxicol 20: 335, 1982

A.Title: Structural studies on a proteinase inhibitor from the sea anemone Stichodactyla sp.

A.Preference number: A27261

A.Accession: A27261

A.Molecule type: protein

A.Residues: 1-28 <MEB>

Query Match 100.0%; Score 20; DB 2; Length 28;

Best Local Similarity 100.0%; Pred. No. 81;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 VLEP 4

DB

4 VLEP 7

RESULT 2

G28027

protein p10 - curled leaved tobacco (fragment)

C.Species: Nicotiana glauca (curled leaved tobacco)

C.Date: 19-MAY-1989 #sequence_revision 13-May-1989 #text_change 11-Jun-2000

C.Accession: G28027

P.Ram, G.; De Looze, M.; Inze, D.; Van Montagu, M.; Van der Kuylen, J.

Proc Natl Acad Sci U S A 84: 4806-4810, 1987

A.Title: Alterations in the phenotype of plant cells studied by RNC terminal amino acid

A.Preference number: A94167

A.Accession: G28027

A.Molecule type: protein

A.Residues: 1-37 <BAU>

C.Superfamily: thaumatin 1

Query Match 100.0%; Score 20; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 114-02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 VLEP 4

DB

29 VLEP 32

ma, A.; Mizutani, M.; Y. Kobayashi, N.; Sawano, T.; Inoue, P.; Fatio, G.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1235-1240, 2001.
 A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A84748; MUID-21311952; PMID:11418146
 A:Accession: E89802
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-63 <KUR>
 A:Cross-references: GR:BA00019, PID:31700078, PID:PA841576 1; GSPRP:GN00149
 A:Experimental source: strain N315
 A:Genetics:
 A:Gene: SAS009

Query Match 100.0% Score 20; DB 2; Length 63;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 35 VLEP 38

RESULT 9
 GR4484
 hypothetical protein At2g07350 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02 Feb 2001 #ext_change 02-Feb-2001
 C:Accession: GR4484
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID-2008487; PMID:10617197
 A:Accession: GR4484
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-68 <STO>
 A:Cross-references: GR:AF000091, MUID:3400759, PID:MA01607 1; GSPRP:GN00130
 A:Gene: At2g07350
 A:Map position: 2

Query Match 100.0% Score 20; DB 2; Length 68;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 6 VLEP 9

RESULT 10
 C72645
 hypothetical protein APES025 - Aeropyrum pernix (strain P1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #ext_change 20-Aug-1999
 C:Accession: C72645
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix.
 A:Reference number: A72450; MUID-0931030; PMID:10382066
 A:Accession: C72645
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <KAW>
 A:Cross-references: GR:AP000060; MUID:AP000060; PID:G5104188; PID:RAA79563 1; PID:d1043349; PID:G510742003
 A:Experimental source: strain K1
 A:Genetics:
 A:Gene: APES025

Query Match 100.0% Score 20; DB 2; Length 81;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 23 VLEP 26

RESULT 13
 742003
 hypothetical protein H3 - human herpesvirus 7 (strain J1)
 C:Species: human herpesvirus 7
 A:Variety: strain J1

Query Match 100.0% Score 20; DB 2; Length 77;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 30 VLEP 33

RESULT 11
 T15286
 hypothetical protein M01D7.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #ext_change 20-Sep-1999
 C:Accession: T15286
 A:Title: The sequence of C. elegans cosmid M01D7.
 A:Reference number: Z18322
 A:Accession: T15286
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-80 <GAT>
 A:Cross-references: EMBL:AF003730; MUID:32105482; PID:32105484; PID:MA01607 1; GSPRP:GN00130
 A:Experimental source: strain Bristol N2; Clone M01D7
 A:Genetics:
 A:Gene: CESP:M01D7.5
 A:Map position: 1
 A:Introns: 19/1; 38/3

Query Match 100.0% Score 20; DB 2; Length 80;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 72 VLEP 75

RESULT 12
 E90324
 hypothetical protein SSC8568 [imported] - Sulfolobus solfataricus (strain 121129)
 C:Species: Sulfolobus solfataricus
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 24-May-2001
 C:Accession: E90324
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID-2008487; PMID:10617197
 A:Accession: E90324
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-81 <KUR>
 A:Cross-references: GR:AE006641; MUID:319814884; PID:MA01607 1; GSPRP:GN00130
 A:Genetics:
 A:Gene: SSC8568

Query Match 100.0% Score 20; DB 2; Length 81;
 Best Local Similarity 100.0% Pred No. 2+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 1 VLEP 4
 Db 23 VLEP 26

RESULT 13
 742003
 hypothetical protein H3 - human herpesvirus 7 (strain J1)
 C:Species: human herpesvirus 7
 A:Variety: strain J1

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 64 Mar-2000
 C/Accession: T41904, 142003
 R/Author: J. Richiadas, C.
 Submitted to the EMBL Data Library, December 1995
 A/Description: Determination and analysis of the complete nucleotide sequence of human H
 A/Reference number: 222022
 A/Accession: T41904
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Cross-references: EMBL 142003
 A/Residues: 1-82 <NIC>
 A/Cross-references: EMBL 142003, PIDN AA054664 1
 A/Experimental source: strain J1
 A/Genetics: GN1
 A/Accession: 142003
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-82 <NIC>
 A/Cross-references: EMBL 142003, PIDN AA054664 1
 A/Experimental source: strain J1
 A/Genetics: <GN1>
 A/Genes: H3
 A/Map position: 1976-4224
 C/Genetics: <GN2>
 A/Genes: H3
 A/Map position: 143023 143271

Query Match 100.0%, Score 20, DB 2, Length 82,
 Best Local Similarity 100.0%, Pref No 2, 7e-02,
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 VLEP 4
 |||||
 DB 19 VLEP 22

RESULT 14
 T19717
 Hypothetical protein 142003 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
 C/Accession: T19717
 R/Baynes, C.
 Submitted to the EMBL Data Library, August 1996
 A/Reference number: 215168
 A/Accession: T19717
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-83 <WIL>
 A/Cross-references: EMBL 278000, PIDN CAP142003, GSPDB 3100423, GESP/C34D1.1
 A/Experimental source: clone C34D1
 C/Genetics:
 A/Genes: GESP-C34D1.1
 A/Map position: 5772
 A/Introns: 3571, 5772

Query Match 100.0%, Score 20, DB 2, Length 23,
 Best Local Similarity 100.0%, Pref No 2, 7e-02,
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 VLEP 4
 |||||
 DB 25 VLEP 29

RESULT 15
 T22022
 Hypothetical protein MTH1799 Methanobacterium thermoautotrophicum (strain Delta H)
 C/Species: Methanobacterium thermoautotrophicum
 C/Date: 03-Oct-1992 #sequence_revision 03-Oct-1992 #ext_change 03-Oct-1992
 C/Accession: C69107
 R/Smith, D.F., Durrant-Brann, L.A., Deloughery, C., Lee, H., Dubois, J., Aldredge, T.,
 Gibb, D., Spudis, P., Viraire, P., Wang, Y., Wierzbicki, Z., Gitsch, P., Ziwni, N.

K., S.J. Church, G.M.J. Daniels, C.G. Mao, J. Rice, P. Noelling, J. Beeve, G.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi
 A/Reference number: A69000; MTH1-08037514; PMID-9471463
 A/Accession: C69107
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-86 <MTH>
 A/Cross-references: 38 AF010331, CP-ACC00006, N11-1261104, F100-AB050255.1, PID:02622981
 A/Experimental source: strain Delta H
 C/Genetics:
 A/Genes: MTH1799

Query Match 100.0%, Score 20, DB 2, Length 66,
 Best Local Similarity 100.0%, Pref No 2, 9e-02,
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 VLEP 4
 |||||
 DB 58 VLEP 61

RESULT 16
 B72296
 Hypothetical protein - Thermotoga maritima (strain MSB8)
 C/Species: Thermotoga maritima
 C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #ext_change 21-Jul-2000
 C/Accession: B72296
 R/Meliss, F.F., Clayton, P.A., Gill, S.P., Quinn, M.L., Dodson, P.J., Haft, D.H., Hickey,
 Garratt, M.M., Stewart, A.M., Gibson, M.D., Pratt, M.S., Phillips, C.A., Richardson, D.,
 C.M.
 Nature 399, 323-329, 1999
 A/Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A/Reference number: A70000, MTH 0000016, PMID-1046471
 A/Accession: B72296
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-89 <ARN>
 A/Cross-references: 38 AF001750, 38 AF000012, MTH 3404120, F100-AB050255.1, PID:040910
 A/Experimental source: strain MSB8
 C/Genetics:
 A/Genes: TM112

Query Match 100.0%, Score 20, DB 2, Length 89,
 Best Local Similarity 100.0%, Pref No 3, 0e-02,
 Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 VLEP 4
 |||||
 DB 78 VLEP 81

RESULT 17
 JN0349
 Bacterial plastocyanin reduction EC1.10.9.117 protein short form barley chloro
 A/Alternate names: cytochrome b6-f complex 17K protein
 C/Species: chloroplast Hordeum vulgare (barley)
 C/Date: 03-Oct-1992 #sequence_revision 03-Oct-1992 #ext_change 03-Jun-2002
 C/Accession: JN0349; S09187
 R/Biffo, V.A., Andreeva, A.V., Peverdastro, S.V., Chakhmakcheva, O.G.
 Bioorg. Khim. 17, 1369-1385, 1991
 A/Title: Nucleotide sequence of the barley chloroplast petP, petC, petF, petH, petB gene
 A/Reference number: JN0349; MTH 0220753, PMID:1464121
 A/Accession: JN0349
 A/Molecule type: DNA
 A/Residues: 1-92 <EF1>
 R/Reverlatte, S.V., Andreeva, A.V., Baryakova, A.A., Chakhmakcheva, O.G., Biffo, V.A.
 Nucleic Acids Res. 17, 2859-2860, 1989
 A/Title: Nucleotide sequence of the 5.2 kbp barley chloroplast DNA fragment, containing
 A/Reference number: S04110, MTH 0220753, PMID:2651887
 A/Accession: S09187
 A/Molecule type: DNA
 A/Residues: 1-92 <FEV>


```

Query Match      100.0%, Score 20, EB 2, Length 99;
Best Local Similarity 100.0%; Pred. No. 34+02;
Matches 4, Conservative 9, Mismatches 0, Indels 0, Gaps 0;

QY      1 VLEP 4
        :|||
Db      22 VLEP 25

```

```

Query Match      100.0%  Score 20;  DE 2;  Length 102;
Best Local Similarity 100.0%  Pred N= 3 5e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps
Qy 1 VLEP 4
    ||||
Db 46 VLEP 49

Search completed: March 5, 2003, 08:34:15
Job time : 48 secs

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OM protein - protein search, using sw model

Run on: Match: 5, 2033, on 27 14, Search time 25 seconds
(without alignments)
5 721 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112992 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: SwissProt_40:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	59	CD3D_BOVIN	Q28072 bos taurus
2	20	100.0	59	PL32_BPME	Q8Y114 bruceella m
3	20	100.0	71	IFI_EEPIN	Q8X314 leptospira
4	20	100.0	92	PPIC_FCOLI	P91559 escherichia
5	20	100.0	92	PPIC_SALTY	Q6L634 salmonella
6	20	100.0	95	YFSS_RHLP	P1G497 thizobium l
7	20	100.0	98	PCWZ_THBAQ	Q889V4 thermus aqu
8	20	100.0	100	V264_EPB01	Q27986 bacterioph
9	20	100.0	103	Y592_CHLPN	Q279W2 chlamydia p
10	20	100.0	106	PL3F_METVA	P14525 methanococ
11	20	100.0	106	PTFD_HOPVJ	P12361 hordeum vul
12	20	100.0	112	YF07_AFCFU	Q28765 archaeglob
13	20	100.0	114	RLA2_EIMTE	Q967Y9 elmeria ten
14	20	100.0	116	MEPT_AICCA	Q52106 acinetobact
15	20	100.0	116	MEPT_ALGSP	P44185 alcaligenes
16	20	100.0	116	MERT_PSEAF	P04140 pseudomonas
17	20	100.0	116	MEPT_PSEFL	Q51769 pseudomonas
18	20	100.0	116	MEPT_SALTI	P04336 salmonella
19	20	100.0	116	MEPT_SEPMA	P13112 sertaria ma
20	20	100.0	116	PEV_HV10Y	P20887 human immun
21	20	100.0	117	DHS0_AFCFU	Q29573 archaeglob
22	20	100.0	120	SYE_STAXY	P77984 staphylococ
23	20	100.0	126	MEPT_ENTAG	P47000 enterobacte
24	20	100.0	129	UMPL_SCHPO	Q74416 schizosacch
25	20	100.0	129	V101_YEAST	P40451 saccharomyc
26	20	100.0	134	WNT1_CHICK	Q91029 gallus gall
27	20	100.0	136	PK16_MAIZE	P08528 zea mays am
28	20	100.0	139	PETD_PEA	P06527 pisum sativ
29	20	100.0	146	YNS1_YEAST	Q00342 saccharomyc
30	20	100.0	147	V336_HSV11	Q00146 ictaluriid h
31	20	100.0	153	1EX1_MOUSE	P46694 mus musculu
32	20	100.0	156	1EX1_HUMAN	P46695 homo sapien
33	20	100.0	157	HFE2_MOUSE	Q54732 mus muscul

34	20	100.0	157	1	HES2_RAT	P35429 rattus norv
35	20	100.0	158	1	WH21_MYXVL	P29450 myxoma viru
36	20	100.0	160	1	PETD_ARATH	P56774 arabidopsis
37	20	100.0	160	1	PETD_MAIZE	P06443 zea mays am
38	20	100.0	160	1	PETD_MAPPO	P06250 marchantia
39	20	100.0	163	1	PETD_MESVI	Q98972 mesocriceta
40	20	100.0	160	1	PETD_ORYSA	P12118 oryza sativ
41	20	100.0	163	1	PETD_SLICE	P11177 silene elae
42	20	100.0	160	1	PETD_TOBAC	P06249 nicotiana gl
43	20	100.0	160	1	PETD_WHEAT	P12119 tritium ae
44	20	100.0	160	1	UI95_HUMAN	Q98971 homo sapien
45	20	100.0	160	1	UI95_MOUSE	Q98972 mus musculu
46	20	100.0	161	1	PETD_GYACA	Q98973 gyrodactylum c
47	20	100.0	167	1	ILVH_MYCAV	Q54434 mycobacteri
48	20	100.0	168	1	ILVH_MYCTU	Q54439 mycobacteri
49	20	100.0	163	1	ILVH_MYCLE	Q23113 mycobacteri
50	20	100.0	171	1	DAPT_RUCAP	Q84590 buchnera ap

ALIGNMENTS

RESULT 1
CD3D_BOVIN
ID CD3D_BOVIN STANDARD; PPT; 59 AA.
AC Q28072;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE T-cell surface glycoprotein CD3 delta chain precursor (T cell receptor
DE T3 delta chain) (Fragment).
GN CD3D.
OS Bos taurus (Bovine).
CC P04VY2; Wataraka, Choudhry, Grantata, Veretkova, Farkasostomi;
CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90269333; PubMed=1971793;
RA Clevers H., Machugh H.D., Bensaïd A., Dunlap S., Baldwin C.L.,
EA Kaushal A., Iams K., Howard C.J., Morrison W.L.;
PT "Identification of a bovine surface antigen uniquely expressed on
RT CD4-CD8-T cell receptor gamma/delta+ T lymphocytes.";
PI Eur J Immunol 20:804-817(1990).
CC -!- FUNCTION: THE CD3 COMPLEX MEDIATES SIGNAL TRANSDUCTION.
CC -!- SUBUNIT: THE TCR/CD3 COMPLEX OF T LYMPHOCYTES CONSISTS OF EITHER
CC A TCR ALPHA/BETA OR TCR GAMMA/DELTA HETERODIMER EXPRESSED AT THE
CC CELL SURFACE WITH THE INVARIANT SUBUNIT OF CD3 EXPRESSED AT THE
CC DELTA, EPSILON, ZETA, AND ETA.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC
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CC or send an email to license@isb.scrib.ch.
CC
CC EMBL: X53269; CAA37367.1;
CC Immunoglobulin domain; T cell; Receptor; Transmembrane, glycoprotein;
DP Signal.
KW SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 59 T CELL SURFACE GLYCOPROTEIN CD3 DELTA
FT CHAIN 22 59 CHAIN
FT DOMAIN 22 59 EXTRACELLULAR (POTENTIAL)
FT CARBOHYD 38 48 N LINKED GLUCNA (POTENTIAL)
FT NON TER 59 59
SQ SEQUENCE 59 AA; 6468 MW; DE050A0A09A540E CPO04;
Query Match 1100, Score 20, TP 1; Length 69;

Best Local Similarity 100.0%, Pred No. 62,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
|||||
DB 20 VLEP 20

RESULT 2

RL32 BRUME
ID P132 BPTYPE STANDARD, PPT, 59 AA
AC Q8YJ14;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 50S ribosomal protein L32.
GN RPL32 OR RMEI0272.
OS Brucella melitensis.
OC Bacteria; Proteobacteria, alpha subdivision, Rhizobiaceae group,
OC Rhizobiaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
SEQUENCE FROM N A
PC STRAIN=16M / ATCC 23456 / Biotype 1;
PX MEDLINE=20020109; PubMed=11756589;
PY DelVecchio V G., Kapral V., Pedkar P.J., Parra G., Mujer C., Los T,
PA Ivarova M., Anderson I., Bhattacharyya A., Lykidis A., Reznik G,
PA Tabianski I., Larson N., D'Souza M., Bernal A., Mazur M., Golestan E.,
RA Selkov E., Elzer P.H., Higgins S., O'Callaghan D., Leeson J.J.,
RA Haselkorn R., Kyriades N., Overbeek R;
RT "The genome sequence of the facultative intracellular pathogen
RT Brucella melitensis.";
EL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002)
CC - SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS

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CC -----
CC EMBL; AB009470; AAL51454.1;
CC InterPro; IPR002677; Ribosomal L32P.
CC Pfam; PF01793; Ribosomal L32P; 1.
CC TIGRFAMs; TIGR01031; rplL32; 1.
CC Ribosomal Protein; Complete Proteome
SQ SEQUENCE 59 AA, 6750 MW, 82122977705528 CP064;

Query Match 100.0%, Score 20; DB 1, Length 59,
Best Local Similarity 100.0%, Pred. No. 62;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
|||||
DB 54 VLEP 57

RESULT 3

IF1_LBPIN
ID IF1_LBPIN STANDARD, PPT, 71 AA.
AC Q9XJ14;
DT 30-MAY-2000 (Rel. 30, Created)
DT 30-MAY-2000 (Rel. 29, Last sequence update)
DT 15-OCT-2001 (Rel. 40, Last annotation update)
DE Translation initiation factor IF-1.
GN INF1.
OS Leptospira interrogans.
OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173,
RN [1]
RP SEQUENCE FROM N.A.

PC STAIN=Serovar Lai;
PX MEDLINE=20000905; PubMed=10620683;
RA Zuerner R.L., Hartkeerl R.A., van de Kemp H., Bal A.E.;
RT "Characterization of the Leptospira interrogans S10-spc-alpha
RT operon.";
PL PEMS Microbiol Lett. 182:303-308(2000)
CC - FUNCTION: NO SPECIFIC FUNCTION HAS SO FAR BEEN ATTRIBUTED TO THIS
CC INITIATION FACTOR. HOWEVER, IT SEEMS TO STIMULATE MORE OR LESS ALL
CC THE ACTIVITIES OF THE OTHER TWO INITIATION FACTORS, IF-2 AND IF-3.
CC - SUBCELLULAR LOCATION: Cytoplasmic
CC - SIMILARITY: BELONGS TO THE IF-1 FAMILY.
CC - SIMILARITY: CONTAINS 1 SI-LIKE DOMAIN.

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CC -----
CC EMBL; AF115283; AAD40605.1;
CC HSP; P02998; IAH9.
CC InterPro; IPR003029; SI.
CC InterPro; IPR004368; TIF-IF1.
CC Pfam; PF00575; SI; 1.
CC SMART; SM00314; SI; 1
CC TIGRFAMs; TIGR00008; infA; 1.
CC PROSITE; PS00832; SI-IF1-TYPE; 1
KW Initiation factor; Protein biosynthesis.
FT INIT MET 0 0 BY SIMILARITY.
FT DOMAIN 1 71 SI-LIKE.
SQ SEQUENCE 71 AA, 8062 MW, 97856461214009 CP064;

Query Match 100.0%, Score 20; DB 1, Length 71;
Best Local Similarity 100.0%, Pred. No. 77;
Matches 4, Conservative 0, Mismatcher 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 12 VLEP 15

RESULT 4

PPIC_ECOLI
ID PPIC_ECOLI STANDARD, PPT, 92 AA.
AC P39159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptidyl prolyl cis-trans isomerase C (EC 5.2.1.9) (PPIase C)
DE (potamase C) (Parvulin).
GN PPIC OF PAPVA CP P377 CP 7559 CP ECS4709.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE.

RX MEDLINE=95010704; PubMed=7925971;
RA Rahfeld J.-U., Ruecknagel F.P., Schelbert B., Ludwig B., Hacker J.,
PA Mann K., Fischer G;
PT "Confirmation of the existence of a third family among
PT peptidyl-prolyl cis/trans isomerases. Amino acid sequence and
PT recombinant production of parvulin.";
RL FEBS Lett. 352:180-184(1994).
RN [2]

PRELIMINARY SEQUENCE FROM N.A

RP STRAIN=K12 / MG1655;
EX MEDLINE=92359234; PubMed=1379743;
RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
PT "Analysis of the Escherichia coli genome. DNA sequence of the region

RT from 84.5 to 86.5 minutes.",
 RL Science 257:771-778(1992).
 RN [3]
 RP REVISIONS, AND IDENTIFICATION.
 RX MEDLINE=95184297; PubMed=7878732;
 RA Fudd K E, Sofia H T, Koonin F V, Plunkett G, III, Lazar S.,
 RA Rouverie P.E.;
 RT "Conserved sequence motifs in bacterial and bacteriophage
 RT chaperonins.";
 RL Trends Biochem Sci 20:14-15(1995)
 RN [4]
 RP SEQUENCE FROM N A
 RC STRAIN=0157:H7 / FNU333 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Ferna N.T., Plunkett G, III, Rutland V, Mau P., Glasner J P,
 RA Rose D J, Mayhew G F, Evans P S, Gregor J, Kirkpatrick H A,
 RA Postai G., Hackett J., Klink S., Rubin A., Shan Y., Miller L.,
 RA Grobeck E J., Davis N W, Lim A, Dimalanta E T., Perazolis F.,
 RA Apudaca J., Mantlatakam T.S., Lin J., Yen G., Schwartz D C,
 RA Welch R.A., Blattner F.R.,
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:520-533(2001)
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=0157:H7 / FNU333/ATCC 700927;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino Y., Onishi M., Furukawa Y., Ishii K., Yokoyama K.,
 RA Han C -G, Onosubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Lida T., Takami H., Honda T., Sakakawa C., Ogisawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K12";
 RL DNA Res 8:11-22(2001)
 RN [6]
 RP SEQUENCE OF 1-21, AND CHARACTERIZATION.
 RX MEDLINE=94216709; PubMed=8163020;
 RA Ratfield J -H., Schierhorn A., Mann K., Fischer G.;
 RT "A novel peptidyl-prolyl cis/trans isomerase from Escherichia coli";
 RL FEBS Lett. 343:65-69(1994)
 CC -1- FUNCTION: PEPTIDYL-PROLYL CIS/TRANS ISOMERASE FROM ESCHERICHIA COLI.
 CC AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND
 CC PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDE SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline
 CC (omega-0)
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic
 CC -1- SIMILARITY: BELONGS TO THE PPI2/PAPVULIN FAMILY OF POTAMASES.
 CC
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 CC
 CC EMBL: S71874; AAR0254.1;
 CC EMBL: M87049; AAA67578.1;
 CC EMBL: AE000454; AAC76780.1;
 CC EMBL: AE005609; AAG58970.1;
 CC EMBL: AF002566; BAB38132.1;
 CC PIR: S45525; S45525.
 CC HSP: Q13526; IPIN.
 CC EcoGene: EG12352; ppiC.
 CC InterPro: IPR000297; Potamase
 CC Pfam: PF00639; Potamase; 1
 CC PROSITE: PS01096; PPI2/PPIASE 1; 1
 CC PROSITE: PS01098; PPI2/PPIASE 2; 1
 KW Isomerase; Potamase; Complete Potamase
 FT INIT MET 0
 SQ SEQUENCE 92 AA: 101; MW: 42148.02; Score 20. DR 1. Length 92.
 Query March 100.00; Score 20. DR 1. Length 92.
 Best Local Similarity 100.00; Prod. No. 1e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 DB 70 VLEP 73
 RESULT 5
 ID_PPI2_SALTY STANDARD; PPT; 92 AA
 AC Q9L6S3;
 RT 16-OCT-2001 (Pel 40, Created)
 DE 15-JUN-2002 (Pel 41, Last annotation update)
 DE Peptidyl-prolyl cis trans isomerase C (PF 5.2.1.8) (PPIase C)
 DE (Potamase C) (Pavulin)
 GN PPI2 OF STM310 OF STM140 OF STY4647.
 OS Salmonella typhimurium, and
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Salmonella.
 CC NCBI TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES: S. typhimurium; STRAIN: LT2 / S350412 / ATCC 14028;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Griwal N., McInerney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston P., Wilson P.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.P., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.P., Holden M.T.G., Sebahia M.,
 RA Parker S., Basham D., Brooks K., Chillingworth T., Connor R.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Paulwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jorgels K.,
 RA Krogan A., Larsen T.S., Leather S., Meele S., Ogata P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skellern J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 CC -1- FUNCTION: PEPTIDYL-PROLYL CIS/TRANS ISOMERASE FROM ESCHERICHIA COLI.
 CC AMINO ACID RESIDUES WITH HYDROPHOBIC SIDE CHAINS LIKE LEUCINE AND
 CC PHENYLALANINE IN THE P1 POSITION OF THE PEPTIDE SUBSTRATE.
 CC -1- CATALYTIC ACTIVITY: peptidylproline (omega-180) = peptidylproline
 CC (omega-0).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PPI2/PAPVULIN FAMILY OF POTAMASES.
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 CC
 CC EMBL: AF333354; AAF33475.1;
 CC EMBL: AE008882; AAC22760.1;
 CC EMBL: AL627279; CAD09407.1;
 CC HSP: Q13526; IPIN.
 CC StyGene: SG23222; ppiC.
 CC InterPro: IPR000297; Potamase.
 CC Pfam: PF00639; Potamase; 1.

```

DE PROSITE, PS01036, PPTC_PP1ASE_1; 1.
DE PROSITE, PS01038, PPTC_PP1ASE_2; 1.
DE PROSITE, PS01039, PPTC_PP1ASE_3; 1.
FW Isomerase; Complete Proteins.
FW INIT MET 0 BY SIMILARITY.
SC SEQUENCE 92 AA, 10107 MW, 1203635PR992904 QP0C4;

Query Match 100.0%; Score 20; DB 1; Length 92;
Best Local Similarity 100.0%; Pred No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 70 VLEP 73

RESULT 6
YFSS_PHLIF STAFFAPP, FFT, 95 AA.
AC P10497;
DE 01-NOV-1999 (Rel. 15, Created)
DE 01-MAY-1993 (Rel. 33, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical protein in pss 5' region (fragment).
DE Rhizobium leguminosarum (biovar phaseoli).
CC Bacteria; Proteobacteria, alpha subdivision; Rhizobiaceae group.
CC Rhizobiaceae; Rhizobium.
QY NCBI_TAXID=185;
RN [1]
PP SEQUENCE FROM N.A.
KU STAFFAPP;
RX MEDLINE=89127126; PubMed 2851702;
RA Borthakur D., Barker R.F., Latchford J.W., Posson L., Johnston A.W.R.;
FT "Analysis of pss genes of Rhizobium leguminosarum required for
FT exopolysaccharide synthesis and nodulation of peas: their primary
FT structure and their interaction with pss and other nodulation
FT genes.";
RL Mol. Gen. Genet. 213:155-162 (1989).
CC - SIMILARITY BELONGS TO THE INOSITOL MONOPHOSPHATASE FAMILY.
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DE RYB1, Y12169, TAA1079 1, ALT_INIT
DE PIR; S03810; S03810.
DE InterPro; IPR000780; Inositol P.
DE Pfam; PF0459; Inositol_P_1.
DE PROSITE; PS00629; IMP 17 PARTIAL.
DE PROSITE; PS00630; IMP 2; 1.
FW Hypothetical protein; Exopolysaccharide synthesis, Nodulation.
FW NON_TER 1
SC SEQUENCE 95 AA; 10149 MW; A3DED804E1BF924B CR264;

Query Match 100.0%; Score 20; DB 1; Length 95;
Best Local Similarity 100.0%; Pred No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 91 VLEP 94

RESULT 7
PP02_THEAQ STANDARD; FFT, 98 AA.
AC Q9EVV4;
DE 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)

DE DNA directed RNA polymerase omega chain (PO 2.7.7.6) (Transcriptase
omega chain) (PNA polymerase omega subunit).
DE PRO..
OS Thermus aquaticus.
CC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
CC Thermaceae; Thermus.
CX NCBI_TAXID=271;
RN [1]
PP SEQUENCE FROM N.A.
RX MEDLINE=20566669; PubMed=11114902;
RA Minakhin L., Nochaev S., Campbell E.A., Severinov K.;
RT "Recombinant Thermus aquaticus RNA polymerase, a new tool for
RT structure-based analysis of transcription.";
RL J. Bacteriol. 183:71-76 (2001).
RN [2]
PP SEQUENCE FROM N.A., SEQUENCE OF 1-10, FUNCTION, AND 3D STRUCTURE
MODELLING.
RX MEDLINE=11107642; PubMed=1158566;
RA Minakhin L., Bhagat S., Running A., Campbell E.A., Darst S.A.,
RA Bhargava R.H., Severinov K.;
FT "Bacterial RNA polymerase subunit omega and eukaryotic PNA polymerase
FT subunit RPB6 are sequence, structural, and functional homologs and
FT promote RNA polymerase assembly.";
PL Proc. Natl. Acad. Sci. U.S.A. 98:892-897 (2001).
CC - FUNCTION: Promotes PNA polymerase assembly. Latches the N- and C-
CC terminal regions of the beta' subunit thereby facilitating its
CC interaction with the beta and alpha subunits.
CC - CATALYTIC ACTIVITY: N nucleoside triphosphate -> N diphosphate +
CC (RNA)(N)
CC - SUBUNIT: CONSISTS OF A SIGMA FACTOR AND THE RNA POLYMERASE ENZYME WHICH
CC IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, 1 BETA' CHAIN AND 1
CC OMEGA CHAIN.
CC - SIMILARITY BELONGS TO THE RNA POLYMERASE OMEGA CHAIN FAMILY.
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DE EMP1, A795830, CAC1949 1; -
DE PDB; 1HQM; 07-FEB-01.
KW Transference; DNA-directed RNA polymerase; Transcription;
FT INIT MET 0
SC SEQUENCE 98 AA; 11494 MW; RE4520AF14PP020FF CR064;

Query Match 100.0%; Score 20; DB 1; Length 98;
Best Local Similarity 100.0%; Pred No. 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 38 VLEP 41

RESULT 8
VG6_BPB03 STANDARD; PRT; 100 AA.
AC Q37886;
DE 15-DEC-1998 (Rel. 37, Created)
DE 15-DEC-1998 (Rel. 37, Last sequence update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DE Early protein GP6.
GN 6
OS Bacteriophage R103
CC Viruses; dsRNA viruses, no RNA stage; Caudovirales; Podoviridae;
CC Phi-29-like viruses.
CX NCBI_TAXID=10778;
RN [1]
PP SEQUENCE FROM N.A

```

PX MEDLINE=96010694, PubMed 936052.
 RA Pecenkova T., Benes V., Paces J., Vitek C., Paces V.;
 RT "Bacteriophage B103, complete DNA sequence of its genome and
 relationship to other Bacillus phages.";
 RL Gene 1993;157:163(1997).
 CC INITIATION OF DNA REPLICATION BY FORMING A MULTIMERIC
 CC NUCLEOPROTEIN COMPLEX AT THE REPLICATION ORIGIN (BY SIMILARITY).
 CC
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 CC
 DR EMBL; X90760; CAA67651.1;
 DP EMBL; X90760; CAA67651.1; ALT_INIT.
 DP EMBL; X90760; CAA67651.1;
 DP TIGR; CP0156;
 DR InterPro; IPR002696; DUF37.
 DR Pfam; PF01809; DUF37.1.
 DR ProDom; PD04425; DUF37.1.
 DR TrpPams; TIGR00279; DUF37.1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 102 AA, 116.7 MW, 28.1307-1406(2000)
 SQ
 Query Match 100.0%; Score 20; PP 1; Length 102;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cys 1 VLEP 4
 Dbs 30 VLEP 33

RESULT 9
 Y592 CHLPPN STANDARD; PRT; 103 AA.
 AC Q97W2; Q97W2P;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 41, Last annotation update)
 DE Hypothetical protein cpn052/cpn156/cpn052.
 GN CPN052, cpn052, cpn156, cpn052
 OS Chlamydia pneumoniae (Chlamydiophila pneumoniae)
 CC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydiophila.
 CX NCBI_TaxID=83558;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=CWL029;
 RX MEDLINE=99206206; PubMed=10197198;
 RA Kalman S., Mitchell W., Marathe P., Lammel C., Fan J., Hyman P.W.,
 PA Olinger L., Griewood J., Davis P.W., Stephens P.S.,
 RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
 RL Nat. Genet. 21:385-394(1999)
 RN [2]
 PP SEQUENCE FROM N.A.
 RC STRAIN=AR39;
 RX MEDLINE=20150255; PubMed=10684935;
 RA Read T.D., Brunham R.C., Shen C., Gill S.P., Heidelberg J.F.,
 RA White O., Hickley E.K., Peterson J., Uitterlinden T., Berry P., Pass S.,
 RA Linher K., Weidman J., Khouri H., Craven P., Bowman C., Dodson P.,
 RA Wilson M., Nelson W., Tarr P., Farnham C., McIntyre S., Salzberg S.L.,
 RA Eisen J., Fraser C.M.;
 RT "Genome sequences of Chlamydia trachomatis McPh and Chlamydia
 RT pneumoniae AR39.";
 RL Nucleic Acids Res. 28:1307-1406(2000)
 RN [3]
 PP SEQUENCE FROM N.A.
 RC STRAIN=J138;
 RX MEDLINE=20101049; PubMed=10871362;
 RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi Y.,
 RA Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.,
 RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
 RT from Japan and CWL029 from USA.";
 RL Nucleic Acids Res. 28:2311-2314(2000)
 CC -1- SIMILARITY: BELONGS TO THE UPF0161 FAMILY.

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 CC
 DR EMBL; AE001643; AAD18731.1;
 DP EMBL; AE002177; AAF32027.1; ALT_INIT.
 DP EMBL; APO02547; RAA98749.1;
 DP TIGR; CP0156;
 DR InterPro; IPR002696; DUF37.
 DR Pfam; PF01809; DUF37.1.
 DR ProDom; PD04425; DUF37.1.
 DR TrpPams; TIGR00279; DUF37.1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 103 AA, 11751 MW, C9CA4853EAL5A7C C9C64;
 SQ
 Query Match 100.0%; Score 20; PP 1; Length 103;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Cys 1 VLEP 4
 Dbs 86 VLEP 89

RESULT 10
 RL3E METVA STANDARD; PRT; 105 AA.
 ID RL3E METVA
 AC P14025;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 30 MAY 2000 (Rel. 20, Last annotation update)
 DE 50S ribosomal protein L30e.
 GN RPL30E.
 OS Methanococcus vannielii.
 CC Archaea; Euryarchaeota; Methanobrevibacter; Methanococcales;
 CC Methanococcaceae; Methanococcus.
 CX NCBI_TaxID=2187;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1224;
 RX MEDLINE=89362493; PubMed=2475640;
 PA Lechner K., Heller G., Boeck A.;
 RT "Organization and nucleotide sequence of a transcriptional unit of
 RT Methanococcus vannielii comprising genes for protein synthesis
 RT elongation factors and ribosomal proteins.";
 RL J. Mol. Evol. 29:20-27(1989)
 RN [2]
 PP -1- SIMILARITY: BELONGS TO THE L30E FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 DR EMBL; X15970; CAA34087.1;
 DP EMBL; X15970; CAA34087.1;
 DP HSSP; P14120; ICN9.
 DR InterPro; IPR000231; Ribosomal_L30e.
 DR InterPro; IPR004038; Ribosomal_L7A.
 DR Pfam; PF01248; Ribosomal_L7Ae; 1.
 DR ProDom; PD04445; Ribosomal_L30e; 1.
 DR PROSITE; PS00789; PIPOSOMAL_L30E; 1.
 DR PROSITE; PS00923; PIPOSOMAL_L30E; 1.
 KW Ribosomal protein.
 SQ SEQUENCE 105 AA, 11515 MW, FICAF330E1598E08 E9C64;
 Query Match 100.0%; Score 20; PP 1; Length 105;

Best local similarity 100.0%, Score 20, DB 1, Length 106;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|
|
|
DB 2: VLEP 24

RESULT 11

PEID_HORVU
ID PEID_HORVU STAMPAP; PRT; 106 AA
AC F12361;
DT 01-OCT-1989 (rel. 12, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Cytochrome B6-F complex subunit 4 (17 kDa polypeptide) (Fragment).
GN PEID.
OS Hordeum vulgare (Barley).
OC Chloroplast.
CC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
CC Equisetata, Magnoliophyta, Liliopsida, Poales, Poaceae, Poaceae,
CC Triticaceae, Hordeum.
CC NCBI_TaxID=4853.
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=V. Sakariis,
RX YESTRINE 8240047, PubMed 2454887.
RA Andreeva A.V., Buryakova A.A., Peverdatto S.V., Chakmakhecheva O.G.,
RA Bishov V.A.;
FT Nucleotide sequence of the 5.2 kbp barley chloroplast DNA fragment,
FT containing psbA-psbH-petB-petD gene cluster.
RL Nucleic Acids Res. 17:2859-2860 (1989).
CC COMMENTS: THE CYTOCHROME B6-F COMPLEX
CC IS A SUBUNIT OF THE MAIN SUBUNIT OF CYTOCHROME B6-F. CYTOCHROME B6-
CC F IS A FLUORESCENT PROTEIN, CYTOCHROME F AND THE RIBOSE PROTEIN
CC BY ALTERNATIVE SPLICING.
CC - SIMILARITY: REFUGES TO THE CYTOCHROME B FAMILY, CORRESPONDS TO THE
CC CARBOXYL END OF MITOCHONDRIAL CYTOCHROME B.
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EMBL: X14107; CAA12269.1;
EMBL: X14107; CAA12269.1;
DR PIR: S04150; S04150.
DR PIR: S09187; S09187.
DR InterPro: IPR000179; Cyt_b_b6.
DR Pfam: PF00032; cytochrome_b6_c1.
DR TIGRFAMs: TIGR01156; cytb6/f1v; 1.
DR PROSITE: PS00193; CYTOCHROME B6_Q; 1.
KW Electron transport; Chloroplast; Photosynthesis; Transmembrane;
KW Alternative splicing.
FT VAPSPLOC 1 17 M35SP33MLKSPPIPI > M3V (IN SHOPT
FT ISOFORM)
FT NON_TER 136 136
SQ SEQUENCE 106 AA; 116/1 MW; 14644AB4047DFD4D CPHK4;
Query Match 100.0%, Score 20, DB 1, Length 106,
Best local similarity 100.0%, Score 20, DB 1, Length 106,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|
|
|
DB 70 VLEP 72

RESULT 12

YF07_ARCFU
ID YF07_ARCFU STANDARD; PRT; 112 AA.
AC O28765;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Hypothetical protein AF1507.
GN AF1507.
OS Archaeoglobus fulgidus.
OC Archaea, Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus
OC NCBI_TaxID=2234;
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
PA Flenk H-P, Clayton P.A., Tomb J.-F., Whitte O., Nelson K.E.,
PA Richard K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
PA Richardson D., Verlayage A.P., Graham D.E., Kyriades N.C.,
PA Fleischmann P.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
PA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
PA Peterson S., Pelech C.I., McNeil L.V., Badger J.H., Glodek A., Zhou L.,
PA Overbeek P., Gocayne J.D., Weidman J.P., McDonald L., Huerbach T.,
PA Cotton M.D., Spillings T., Artach P., Kaine P.P., Sykes S.M.,
PA Sadow P.W., D'Andrea V.P., Bowman C., Fujii C., Garland S.A.,
PA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
PA Venter J.C.;
FT The complete genome sequence of the hyperthermophilic, sulphate-
FT reducing archaeon Archaeoglobus fulgidus.
RL Nature 390:364-370 (1997).

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EMBL: AF000998; AAB89743.1;
DR TIGR: AF1507;
KW Hypothetical protein; Complete proteome
SQ SEQUENCE 112 AA; 13069 MW; 6C820E43E141B42B CRC64;

Query Match 100.0%, Score 20, DB 1, Length 112,
Best local similarity 100.0%, Score 20, DB 1, Length 112,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|
|
|
DB 82 VLEP 85

RESULT 13

RLA2_EIMTE
ID RLA2_EIMTE STANDARD; PRT; 114 AA.
AC Q967Y9;
DT 15-JUN-2002 (rel. 41, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE 60S acidic ribosomal protein P2.
OS Eimeria tenella
OC Eukaryota; Alveolata; Apicomplexa, Coccidia, Eimeriida, Eimeriidae;
OC Eimeria.
OC NCBI_TaxID=5902,
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=PAPT38;
RA Labbe M., Pery P.;
FT "Molecular cloning of a cDNA encoding an acidic ribosomal protein P2
RT of Eimeria tenella."
PL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

CC -- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
 CC PROTEIN SYNTHESIS (BY SIMILARITY).
 CC -- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
 CC SUBUNIT (BY SIMILARITY).
 CC -- PTM: PHOSPHORYLATED (BY SIMILARITY).
 CC -- SIMILARITY: RELATES TO THE VLEP FAMILY OF RIBOSOMAL PROTEINS
 CC
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 CC
 CC EMBL: AF353514; AAK38885.1; ALT_INIT.
 CC InterPro: IPR001813; 60s_ribosomal.
 CC Pfam: PF00424; 60s_ribosomal; 1.
 CC Ribosomal Protein; Phosphorylation.
 CC SQ SEQUENCE 114 AA; 11444 MW; 4709G3C5C9078AA9 CRC64;
 CC
 CC Query Match 100.0%; Score 20; DB 1; Length 114;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 VLEP 4
 CC DB 26 VLEP 29
 CC
 CC RESULT 14
 CC MERT ACICA STANDARD; PRT; 116 AA
 CC ID MERT ACICA
 CC AC Q52106;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Mercutic transport protein (Mercury ion transport protein).
 CC GN MERT.
 CC OS Acinetobacter calcoaceticus.
 CC OG Plasmid pKLH2.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae.
 CC OC Acinetobacter.
 CC OX NCBI_TaxID=471;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC FX MEDLINE-94134837; PubMed 8302940.
 CC PA Kholodil G.Y., Iomovskaya O.L., Gorlenko Z.M., Mindlin S.Z.,
 CC Yuriyeva O.V., Nikiforov V.G.;
 CC FT "Molecular characterization of an aberrant mercury resistance
 CC transposable element from an environmental Acinetobacter strain."
 CC RL Plasmid 30:303-308(1993).
 CC -- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
 CC FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE
 CC (MER).
 CC -- SURCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC
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 CC
 CC EMBL: AF213017; AAA19679.1;
 CC InterPro: IPR003457; Transprt_Mert.
 CC Pfam: PF02411; Mert; 1.
 CC KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
 CC Transmembrane.
 CC FT TRANSMEM 16 36 POTENTIAL.
 CC FT TRANSMEM 46 66 POTENTIAL.
 CC FT METAL 16 36 POTENTIAL.
 CC FT METAL 46 66 POTENTIAL.

FT TRANSMEM 94 114 POTENTIAL.
 FT METAL 24 24 HG(2+) (BY SIMILARITY).
 FT METAL 25 25 HG(2+) (BY SIMILARITY).
 FT METAL 76 76 HG(2+) (BY SIMILARITY).
 FT METAL 82 82 HG(2+) (BY SIMILARITY).
 SQ SEQUENCE 116 AA; 12509 MW; 290A3C36234BAC33 CRC64;
 CC
 CC Query Match 100.0%; Score 20; DB 1; Length 116;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 VLEP 4
 CC DB 46 VLEP 49
 CC
 CC RESULT 15
 CC MERT ALCSP STANDARD; PRT; 116 AA.
 CC ID MERT ALCSP
 CC AC P94185;
 CC DT 01-NOV-1997 (Rel. 35, Created)
 CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
 CC DT 15-JUN-1999 (Rel. 38, Last annotation update)
 CC DE Mercutic transport protein (Mercury ion transport protein).
 CC GN MERT.
 CC OS Alcaligenes sp.
 CC OG Plasmid IncH12 pMER610.
 CC OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
 CC OC Alcaligenes.
 CC OX NCBI_TaxID=512;
 CC [1]
 CC RP SEQUENCE FROM N.A.
 CC PA Nikiforov V., Yuriyeva O., Kholodil G., Moraxella Z.,
 CC Kalyaeva E., Mindlin S.;
 CC RL Submitted (ECC-1996) to the EMBL/GenBank/DBJ databases.
 CC -- FUNCTION: INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
 CC FROM THE PERIPLASMIC MERP PROTEIN TO THE MERCURIC REDUCTASE
 CC (MER).
 CC -- SURCELLULAR LOCATION: Integral membrane protein. Inner membrane
 CC (By similarity).
 CC
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 CC
 CC EMBL: Y08993; CAA70196.1;
 CC InterPro: IPR003457; Transprt_Mert.
 CC Pfam: PF02411; Mert; 1.
 CC KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid;
 CC Transmembrane.
 CC FT TRANSMEM 16 36 POTENTIAL.
 CC FT TRANSMEM 46 66 POTENTIAL.
 CC FT METAL 24 24 HG(2+) (BY SIMILARITY).
 CC FT METAL 25 25 HG(2+) (BY SIMILARITY).
 CC FT METAL 76 76 HG(2+) (BY SIMILARITY).
 CC FT METAL 82 82 HG(2+) (BY SIMILARITY).
 SQ SEQUENCE 116 AA; 12509 MW; AAE13C36234BAC33 CRC64;
 CC
 CC Query Match 100.0%; Score 20; DB 1; Length 116;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 CC Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 1 VLEP 4
 CC DB 46 VLEP 49
 CC
 CC RESULT 16

PA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 PT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX SPECIES=S.flexneri;
 RX MEDLINE=85014891; PubMed=6091128;
 RA Mista T.K., Brown N.L., Fritzing D.C., Pridmore R.D., Barnes W.M.,
 RA Haberstroh L., Silver S.;
 RT "Mercuric ion-resistance operons of plasmid p100 and transposon
 PT Tn501: the beginning of the operon including the regulatory region
 RT and the first two structural genes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:5975-5979(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX SPECIES=S.flexneri; PLASMID=IncFII NP1; TRANSPOSON=Trn21;
 RX MEDLINE=85159407; PubMed=6530603;
 RA Battineau P., Gilbey P., Jackson W.J., Jones C.S., Summers A.C.,
 RA Wisdom S.;
 RT "The DNA sequence of the mercury resistance operon of the IncFII
 PT plasmid NP1.";
 RL J. Mol. Appl. Genet. 2:601-619(1984).
 RN [3]
 RP FUNCTION INVOLVED: IN MERCUPTIC TRANSP. PT PASSES A HG(2+) ION
 CC FROM THE PERIPLASMIC MEPP PROTEIN TO THE MERCURIC REDUCTASE
 CC (MERA).
 CC -- SUPERCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC
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 CC
 DR EMBL; AL513381; CAP00916.1;
 DR EMBL; K03089; AAR59075.1;
 DR PIR; A04458; QCBPHT
 DR InterPro: IPR003457; Transprt_MerT.
 DR Pfam; PF02411; MerT.1
 KW Transprt; Mercuric resistance; Inner membrane, Mercury, Plasmid,
 FT Transmembrane; Transposable element; Complete proteome.
 FT TRANSMEM 16 36 POTENTIAL.
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT METAL 24 24 HG(2+) (POTENTIAL).
 FT METAL 25 25 HG(2+) (POTENTIAL).
 FT METAL 76 76 HG(2+) (POTENTIAL).
 FT METAL 82 82 HG(2+) (POTENTIAL).
 SQ SEQUENCE 116 AA; 1251 MW; 8CF0744F4B0F6EB4 CRC64,
 Query Match 100.0%; Score 20; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1 to 100;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 DB 46 VLEP 49
 RESULT 19
 MERT_SERMA STANDARD; PRT; 116 AA.
 AC P13112;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-JAN-1990 (rel. 13, Last sequence update)
 DT 01-NOV-1997 (rel. 35, Last annotation update)
 DE Mercuric transport protein (Mercury ion transport protein)
 GS MERT.
 OS Serratia marcescens.
 OG Plasmid pD01358.

CC Bacteria, Proteobacteria; gamma subdivision, Enterobacteriaceae;
 CC Serratia.
 OK NCBI_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89327136; PubMed=2666393;
 RA Nucleifora G., Chu L., Silver S., Misra T.K.;
 RT "Mercury operon regulation by the merP gene of the organomercurial
 RT resistance system of plasmid pD01358.";
 RL J. Bacteriol. 171:4241-4247(1989).
 CC -- FUNCTION INVOLVED IN MERCURIC TRANSPORT. PASSES A HG(2+) ION
 CC FROM THE PERIPLASMIC MEPP PROTEIN TO THE MERCURIC REDUCTASE
 CC (MERA).
 CC -- SUPERCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC
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 CC
 DR EMBL; M42240; AAA98122.1;
 DR PIR; B33858; B33858.
 DR InterPro: IPR003457; Transprt_MerT.
 DR Pfam; PF02411; MerT.1
 KW Transprt; Transposable element; Mercuric resistance; Inner membrane;
 FT Mercury; Plasmid; Transmembrane.
 FT TRANSMEM 16 36 POTENTIAL.
 FT TRANSMEM 46 66 POTENTIAL.
 FT TRANSMEM 94 114 POTENTIAL.
 FT METAL 24 24 HG(2+) (POTENTIAL).
 FT METAL 25 25 HG(2+) (POTENTIAL).
 FT METAL 76 76 HG(2+) (POTENTIAL).
 FT METAL 82 82 HG(2+) (POTENTIAL).
 SQ SEQUENCE 116 AA; 13511 MW; 4BE13264E31A79E CRC64;
 Query Match 100.0%; Score 20; DB 1; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1 to 100;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 DB 46 VLEP 49
 RESULT 20
 REV_HV10Y
 ID REV_HV10Y STANDARD; PRT; 116 AA.
 AC P20887;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-FEB-1991 (rel. 17, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE REV protein (Anti-repression transactivator protein) (ARTVTPS).
 GN REV.
 OS Human immunodeficiency virus type 1 (OVI isolate) (HIV-1).
 CC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OK NCBI_TaxID=11699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148544; PubMed=2559749;
 RA Huet T., Dazza M.C., Brun-Vezinet F., Poellans G.F., Wain-Hobson S.;
 RT "A highly defective HIV 1 strain isolated from a healthy Gabonese
 RT individual presenting an atypical western blot.";
 RL AIDS 3:707-715(1989).
 CC -- FUNCTION REV APPEARS TO ACT POST TRANSCRIPTIONALLY TO REPRESS
 CC NEGATIVE REPRESSION OF gag AND env PRODUCTION.
 CC -- SUPERCELLULAR LOCATION: Nuclear, accumulates in the nucleoli.
 CC -- PPM: PHOSPHOPOTIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
 CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
 CC -- MISCELLANEOUS: THE OVI ISOLATE WAS TAKEN FROM THE BLOOD OF A
 CC HEALTHY GABONESE INDIVIDUAL.

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CC or send an email to license@isb-sib.ch).

DR EMBL; M26727; AA083366.1; -
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SQ SEQUENCE 112 AA, 13058 MW, 30625.02235647170 pI, 7.654,

Query Match 100.0%, Score 20, DB 1, Length 116;
Best Local Similarity 100.0%; Pref No. 1.3e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
DB 109 VLEP 112

RESULT 21
DRSD ARCFU
ID CHS2-APCFU STANDARD, PFT, 117 AA
AC 029573;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Succinate dehydrogenase hydrophobic membrane anchor protein.
GN SCDH-OP AF0684.
OS Archaeoglobus fulgidus
OC Archaea, Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus
OX NCBI_TaxID=2234,
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Fleck H.E., Clayton P.A., Toml J.F., White C., Nelson J.E.,
PA Ketchum K.A., Dodson P.J., Gwin M., Hickey E.K., Peterson J.D.,
PA Richardson D.L., Kesteven A.P., Graham D.E., Kyrtides N.C.,
PA Fleckmann P.D., Quackenbush J., Lee N.H., Sutton G.G., Gili S.,
PA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
PA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodex A., Zhou L.,
FA Svetlichny F., Gwynne D., Weidman J.F., MacDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.",
RL Nature 390:364-370(1997).

CC -1- FUNCTION: PUTATIVE HYDROPHOBIC COMPONENT OF THE SUCCINATE
CC FERRIVOXENASE COMPLEX. COULD BE REQUIRED TO ANCHOR THE CATALYTIC
CC COMPONENTS TO THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SUBUNIT: PART OF AN ENZYME COMPLEX CONTAINING FOUR SUBUNITS A
CC FLAVOPROTEIN, AN IRON-SULFUR, CYTOCHROME B-556, AND AN HYDROPHOBIC
CC ANCHOR PROTEIN (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable)

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DR EMBL; AE001057; AAB90554.1; -
DR TIGR; AF0684; -
DR InterPro; IPR000701; Sdh_cyt.
DR Pfam; PF01127; Sdh_cyt; 1.
KW Tricarboxylic acid cycle; Electron transport; Heme; Transmembrane;
KW Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 97 117 POTENTIAL.
FT BINDING 73 73 HEME (BY SIMILARITY).
SQ SEQUENCE 117 AA, 13100 MW, 7289CF914F52B7D3 CF64;

Query Match 100.0%, Score 20, DB 1, Length 117;
Best Local Similarity 100.0%; Pref No. 1.3e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
DB 10 VLEP 13

RESULT 22
SYE STAXY STANDARD, PFT, 120 AA.
ID AC P77984;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16 OCT-2001 (Rel. 40, Last annotation update)
DE Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate-tRNA ligase)
DE (Glurs) (Fragment).
GN GLTX.
OS Staphylococcus xylosus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1388;
RN [1]
PP SEQUENCE FROM N.A.
RC STRAIN=DSM 20267 / Isolate CSA;
RX MEDLINE=97237691; PubMed=9084146;
RA Fiegler H., Brueckner R.;
RT "Identification of the serine acetyltransferase gene of Staphylococcus
RT xylosus.",
RL FEMS Microbiol. Lett. 149:181-187(1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
CC diphosphate + L-glutamyl-tRNA(Glu).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.

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DR EMBL; Y07614; CAA68866.1; -
DR InterPro; IPR000324; Glu-tRNA-synt_1
DR Pfam; PF00749; tRNA-synt_1c; 1.
DR PROSITE; PS00178; AA-TRNA-LIGASE_1; PARTIAL.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT NON_TER 1
SQ SEQUENCE 120 AA, 13638 MW, 6A2CE7FC1332C763 CF064;

Query Match 100.0%, Score 20, DB 1, Length 120;
Best Local Similarity 100.0%; Pref No. 1.4e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
DB 56 VLEP 59

```

RESULT 23
MERT_ENTAG
ID MERT_ENTAG STANDARD; PPT: 126 AA
AC P94760;
DT 01-NOV-1997 (rel 35, Last sequence update)
DT 01-NOV-1997 (rel 35, Last sequence update)
DT 15-JUN-2002 (rel 41, Last annotation update)
DE Mercuric transport protein (Mercury ion transport protein)
GN MERT.
OS Enterobacter agglomerans (Pantoea agglomerans).
OG Bacteria; Proteobacteria; Gamma subdivision; Enterobacteriaceae;
OC Pantoea.
OX NCBI_TaxID=549;
RN [1]_TaxID=549;
RP SEQUENCE FROM N.A.; PubMed=9159519;
RX MEDLINE=9159519; PubMed=9159519;
RA Yurteva O., Kholodil G., Minakhin L., Gorlenko Z., Kalyaeva E.,
FA Mindlin S., Nikiforov V.;
RT "Intercontinental spread of promiscuous mercury-resistance
transposons in environmental bacteria.";
RL Mol. Microbiol. 24:321-329(1997)
CC FUNCTION: INVOLVED IN MEROPHILIC TRANSPORT. PASSES A HG(2+) ION
FROM THE PERIPLASMIC MEMP PROTEIN TO THE MEMBRANE PROTEINASE
(MERA)
CC FROM THE PERIPLASMIC LOCATION. INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE.
CC (BY SIMILARITY)
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CC
DR EMBL; Y08992; CAA70186.1;
DR InterPro; IPR003457; Transprt_Mert.
DR Pfam; PF02411; MERT; 1.
KW Transport; Mercuric resistance; Inner membrane; Mercury; Plasmid,
Transmembrane.
FT Transmem 26 46 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 104 124 POTENTIAL.
FT METAL 34 34 HG(2+) (BY SIMILARITY).
FT METAL 35 35 HG(2+) (BY SIMILARITY).
FT METAL 86 86 HG(2+) (BY SIMILARITY).
FT METAL 92 92 HG(2+) (BY SIMILARITY).
SQ SEQUENCE 126 AA; 13664 MW; 20484RPF5A7D0F CPG64.
Query Match 100.0%; Score 20; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 56 VLEP 59
RESULT 24
UMPL_SCHPO
ID UMP1_SCHPO STANDARD; PPT: 129 AA.
AC O74416;
DT 16-OCT-2001 (rel 40, Created)
DT 16-OCT-2001 (rel 40, Last sequence update)
DT 15-JUN-2002 (rel 41, Last annotation update)
DE Putative proteasome maturation factor umpl
GN SPCC14010.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.

```

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OX NCBI_TaxID=4896;
RN [1]_TaxID=4896;
RP SEQUENCE FROM N.A.
PC STRAIN=972;
RX MEDLINE=21848401; PubMed11859360;
PA Wood V., Williams P., Pajandream M.A., Lyne M., Lyne P., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor P., Cronin A., Davis P., Bellwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hildalgo T., Hudson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt C., Gargis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
FA Money F., Moule S., Mungall F., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitz E.,
RA Rutherford K., Putter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Stevens S., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
PA Woodward J., Volckaert G., Aert P., Robben J., Grympeprez B.,
RA Welljens I., Vanstraelen E., Pieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl P., Hilbert H.,
RA Beyer M., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Drenth S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thorpe G.,
PA Daga P., Cruzado I., Gimenez J., Sanchez M., del Roy P., Benito L.,
PA Dominguez A., Revuelta J.L., Marenc G., Arretzky J., Feschky S.L.,
RA Cerutti L., Lowe T., McCombie W.F., Paulsen I., Potashkin J.,
RA Shpakowski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
PL Nature 415:871-880(2002).
CC FUNCTION: SHORT-LIVED TRAPPORE PRESENT IN THE PERIPLASMIC FORM OF
THE SCS PROTEASOME AND ABSENT IN THE MATURE COMPLEX. REQUIRED FOR
THE CORRECT ASSEMBLY AND ENZYMIC ACTIVATION OF THE PROTEASOME
(BY SIMILARITY).
CC
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CC
CC EMBL; AL031518; CAA20656.1;
KW Hypothetical protein; Proteasome; Chaperone.
DP Hypothetical protein; Proteasome; Chaperone.
SQ SEQUENCE 129 AA; 14661 MW; 36CAE66B33BE4C1 CPG64;
Query Match 100.0%; Score 20; DB 1; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 21 VLEP 24
RESULT 25
V101_YEAST
ID V101_YEAST STANDARD; PPT: 129 AA.
AC P40461;
DT 01-FEB-1995 (rel 31, Created)
DT 01-FEB-1995 (rel 31, Last sequence update)
DT 01-OCT-1996 (rel 34, Last annotation update)
DE Hypothetical 14.4 kDa protein in OCT2-AX12 intergenic region.
GN V11141W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]_TaxID=4932;
RP SEQUENCE FROM N.A.
PC STRAIN=S288C / AB972;

```

PA Barrell B.G., Badcock K., Rankier A.T., Bowman S., Brown D.,
 RA Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
 RA Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
 PA Louis F., Lye G., Moule S., Moule T., Odell C., Pearson D.,
 PA Pajandream M.A., Piles L., Powley N., Skelton J., Smith V.,
 RA Walsh S.V., Whitehead S.;
 PL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases
 CC -----
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 CC -----
 DR EMBL; Z38059; CAA86137.1; -;
 DR PIR; S48393; S48393.
 DP SGD; S0001403; YII141W.
 KW Hypothetical protein.
 SQ SEQUENCE 125 AA; 14437 MW; 4A1891980F5BF77R CEC64;

 Query Match 100.0%; Score 20; DB 1; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.Se+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0,

 QY 1 VLEP 4
 DB 7 VLEP 10

Search completed: March 5, 2003, 09:32:46
 Job time : 31 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 5, 2003, 04:40:05 : Search time 24 seconds
(without alignments)
28 428 Million cell updates/sec

Title: US-09-732-411-15
Perfect score: 20
Sequence: 1 VLEP 4

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671500 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671500

Minimum DR seq length: 5

Maximum DR seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 50 summaries

Database:

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rviro:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	20	100.0	24	5	Q9RM55	Q9RM55 chione conc
2	20	100.0	26	5	Q9RM52	Q9RM52 toniliform
3	20	100.0	30	11	Q9WJ19	Q9WJ19 gallus gall
4	20	100.0	43	12	Q9WJ36	Q9WJ36 canine dist
5	20	100.0	47	8	Q9SP47	Q9SP47 spartina an
6	20	100.0	47	9	Q9SP46	Q9SP46 spartina an
7	20	100.0	47	9	Q9SP45	Q9SP45 pseudomonas
8	20	100.0	52	2	Q9PWW3	Q9PWW3 homo sapien
9	20	100.0	55	4	Q9PFW4	Q9PFW4 calicivirus
10	20	100.0	58	12	Q9AC31	Q9AC31 calicivirus
11	20	100.0	58	12	Q9AC32	Q9AC32 chilo iride
12	20	100.0	61	12	Q95728	Q95728 chilo iride
13	20	100.0	62	17	Q97US6	Q97US6 sulfolobus
14	20	100.0	63	10	Q9FEX8	Q9FEX8 hordeum vul
15	20	100.0	63	16	Q99WL3	Q99WL3 staphylococ
16	20	100.0	64	2	Q96120	Q96120 methylobact

17	20	100.0	65	3	Q14380	Q14380 schizosacch
18	20	100.0	68	16	Q9CCV7	Q9CCV7 arab thieric
19	20	100.0	71	13	Q9CWW7	Q9CWW7 cestusiv co
20	20	100.0	74	11	Q9CJ82	Q9CJ82 mus musculu
21	20	100.0	77	16	Q9CJ80	Q9CJ80 streptomyce
22	20	100.0	77	17	Q9CJ81	Q9CJ81 streptomyce
23	20	100.0	79	11	Q9CJ85	Q9CJ85 ratie novu
24	20	100.0	80	5	Q9CJ86	Q9CJ86 caenothabid
25	20	100.0	81	12	Q9CJ86	Q9CJ86 canipe dist
26	20	100.0	81	17	Q9CJ86	Q9CJ86 canipe dist
27	20	100.0	82	8	Q9CJ86	Q9CJ86 canipe dist
28	20	100.0	82	12	Q9CJ86	Q9CJ86 canipe dist
29	20	100.0	83	5	Q18436	Q18436 human hepe
30	20	100.0	83	16	Q9CJ85	Q9CJ85 streptomyce
31	20	100.0	84	12	Q9CJ86	Q9CJ86 canipe dist
32	20	100.0	85	9	Q9CJ86	Q9CJ86 canipe dist
33	20	100.0	86	12	Q9CJ86	Q9CJ86 canipe dist
34	20	100.0	87	17	Q9CJ86	Q9CJ86 canipe dist
35	20	100.0	88	4	Q9CJ86	Q9CJ86 canipe dist
36	20	100.0	89	16	Q9CJ86	Q9CJ86 canipe dist
37	20	100.0	90	15	Q9CJ86	Q9CJ86 canipe dist
38	20	100.0	90	15	Q9CJ86	Q9CJ86 canipe dist
39	20	100.0	90	15	Q9CJ86	Q9CJ86 canipe dist
40	20	100.0	90	15	Q9CJ86	Q9CJ86 canipe dist
41	20	100.0	91	6	Q9CJ86	Q9CJ86 canipe dist
42	20	100.0	93	2	Q9CJ86	Q9CJ86 canipe dist
43	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
44	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
45	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
46	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
47	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
48	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
49	20	100.0	93	5	Q9CJ86	Q9CJ86 canipe dist
50	20	100.0	94	10	Q9CJ86	Q9CJ86 canipe dist

ALIGNMENTS

RESULT 1

ID	Q9RM55	PRELIMINARY;	PRT;	25 AA.
AC	Q9RM55;			
DT	01-JUN-2001 (TREMURel 17, Created)			
DT	01-JUN-2001 (TREMURel 17, Last sequence update)			
DT	01-JUN-2001 (TREMURel 17, Last annotation update)			
DE	LINE-like reverse transcriptase (Fragment).			
OS	Chione cancellata.			
CC	Eukaryota; Metazoa; Mollusca; Bivalvia; Heterodonta; Veneroida;			
OC	Veneroidae; Veneridae; Chione.			
CX	NCBI TaxID:145464.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
PT	TRANSPORIN LST-11 PETROTRANSPORIN;			
RX	MEDLINE=20570504; PubMed=11121049;			
RA	Arkhipova I., Meselson M.;			
RT	"Transposable elements in sexual and asexual taxa";			
PL	Proc. Natl. Acad. Sci. U.S.A. 97:14473-14477(2000).			
DR	EMBL: AY013938; AAC59933.1; ...			
KW	RNA-directed DNA polymerase.			
FT	NON TER 1			
FT	NON TER 25			
SQ	SEQUENCE 25 AA, 2752 MW, 113515FFC4A42A7 Q9RM55;			

Query Match: 100.0%, Score 20, DP 5, Length 25;

Best Local Similarity: 100.0%, Prod No. 2.2e+02;

Matches: 4; Conservativ: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 VLEP 4

Db 2 VLEP 5

```

RESULT 2
Q9WNJ6 PRELIMINARY, PRT, 36 AA.
AC Q9WNJ6
DT 01-NOV-1999 (TRENBLrel, 12, Created)
DT 01-NOV-1999 (TRENBLrel, 12, Last sequence update)
DT 01-JUN-2001 (TRENBLrel, 17, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales.
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
CX NCBI_TaxID:1232,
RN [1]
PP SEQUENCE FROM N.A.
RA Pickel J., Czupalla O.;
RT "Canine distemper virus in a badger (Meles meles).";
PL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DP EVB1, AF150066, AAC30054.2;
DR InterPro: IPR000776; Fusion gly.
DR Pfam: PF00523; fusion_gly; 1.
FT NON_TER 1 43
FT NON_TER 43 43
SQ SEQUENCE 43 AA, 4724 MW, DA940A5C1C73A9C9 CPC64;

Query Match 100.0%; Score 20, DB 12, Length 43;
Best Local Similarity 100.0%; Pred No. 2 0.02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 30 VLEP 33

RESULT 5
Q95F87 PRELIMINARY, PRT, 47 AA.
AC Q95F87
DT 01-DEC-2001 (TRENBLrel, 19, Created)
DT 01-DEC-1991 (TRENBLrel, 19, Last sequence update)
DT 01-MAR-2002 (TRENBLrel, 20, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Spartina alterniflora (smooth cordgrass).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Etrypophyta; Tracheophyta.
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Chloridaceae; Cyndocneae; Spartina
CX NCBI_TaxID:29706,
RN [1]
PP SEQUENCE FROM N.A.
RA Baume A., Ainouche M.L., Levasseur J.-E.;
RT "Molecular investigations in populations of Spartina anglica L. E.
ET Hubbard invading coastal Brittany (France).";
PL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF276959, AAK71924.1;
DR InterPro: IPR000114; Ribosomal L16.
DR Pfam: PF00252; Ribosomal_L16; 1
KW Chloroplast.
FT NON_TER 1 47
FT NON_TER 47 47
SQ SEQUENCE 47 AA, 5679 MW, DEFE09A67537721 CPC64;

Query Match 100.0%; Score 20, DB 8, Length 47;
Best Local Similarity 100.0%; Pred No. 4 0.02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 35 VLEP 38

RESULT 6
Q95F86 PRELIMINARY, PRT, 47 AA.
AC Q95F86
ID Q9WNJ6

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DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 DE Ribosomal protein L16 (Fragment)
 GN RPL16.
 OS Spartina anglica
 OG Chloroplast.
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
 OC Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade;
 OC Chloridoideae, Cynodonteae, Spartina.
 OX NCBI_TaxID=49786;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.,
 PT "Molecular investigations in populations of *Spartina anglica* C. E.
 RT Hubbard invading coastal Brittany (France)."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF276969; AAK71926.1;
 DR InterPro: IPR000114; Ribosomal_L16
 DR Pfam: PF00252; Ribosomal_L16; 1.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 47 47
 SQ SEQUENCE 47 AA; 6670 MW; 108930AA67C7721 7564;

Query Match 100.0%; Score 20; DP 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 35 VLEP 38

RESULT 7

Q95F85 PRELIMINARY; PRT; 47 AA.
 AC Q95F85;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 20, Last annotation update)
 DE Ribosomal protein L16 (Fragment)
 GN RPL16.
 OS Spartina maritima.
 OG Chloroplast.
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
 OC Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade;
 OC Chloridoideae, Cynodonteae, Spartina.
 OX NCBI_TaxID=49786;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA Baumeil A., Ainouche M.L., Levasseur J.-E.,
 PT "Molecular investigations in populations of *Spartina anglica* C. E.
 RT Hubbard invading coastal Brittany (France)."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF276970; AAK71926.1;
 DR InterPro: IPR000114; Ribosomal_L16.
 DR Pfam: PF00252; Ribosomal_L16; 1.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 47 47
 SQ SEQUENCE 47 AA; 6674 MW; 108930AA67C7721 7564;

Query Match 100.0%; Score 20; DP 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 35 VLEP 38

RESULT 8

Q95WW3 PRELIMINARY; PRT; 52 AA.
 AC Q95WW3;
 DT 01-OCT-2000 (TRENBLREL. 15, Created)
 DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
 DT 01-MAR-2002 (TRENBLREL. 21, Last annotation update)
 DE Mercuroic ion transport protein (Fragment)
 GN MEPT.
 OS Pseudomonas putida.
 OC Bacteria, Proteobacteria, gamma subdivision, Pseudomonadaceae,
 OC Pseudomonas.
 OX NCBI_TaxID=303;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA STEINMETZ J. P., TRANSPONSON-TN5041D;
 PA Khodadadi G. Y., Michelin S. Z., Gallardo C. M., Bass L. A., Fajardo P. S.,
 RA Nikiforov V.;
 RT "Host-dependent transposition of Tn5041."
 RT Puss J. Genet. 32:365-371(2000).
 DR EMBL: Y18977; CAB8562.1;
 DR InterPro: IPR001457; Transprt_MerT.
 DR Pfam: PF02411; MerT; 1.
 FT NON_TER 52 52
 SQ SEQUENCE 52 AA; 5200 MW; E6708E2432B912 7564;

Query Match 100.0%; Score 20; DP 2; Length 52;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 46 VLEP 49

RESULT 9

Q96FP4 PRELIMINARY; PRT; 55 AA.
 AC Q96FP4;
 DT 01-DEC-2001 (TRENBLREL. 19, Created)
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE Unknown (protein for MGC:18216).
 OS Homo sapiens (Human).
 OC Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
 OC Mammalia, Eutheria, Primates, Catarrhini, Homnidae, Homo.
 OX NCBI_TaxID=9606,
 RN [1]
 PP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RT Submitted (JUL 2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC010607; AAH10607.1;
 SQ SEQUENCE 55 AA; 6011 MW; 191A7512A79B7EE 7564;

Query Match 100.0%; Score 20; DP 4; Length 55;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 6 VLEP 9

RESULT 10

Q39631 PRELIMINARY; PRT; 58 AA.
 AC Q39631;
 DT 01-JAN-1998 (TRENBLREL. 05, Created)
 DT 01-JAN-1998 (TRENBLREL. 05, Last sequence update)
 DT 01-OCT-2001 (TRENBLREL. 18, Last annotation update)
 DE Capsid protein (Fragment).
 OS Calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae.

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OX NCBI_TaxID=11975;
RN [1]_TaxID=11975;
FC SEQUENCE FROM N.A.
RC STRAIN B453/92/UX.
RA MEDLINE=97279118, PubMed=9131452,
RX Green S.M., Lambden P.R., Owen G.A., Clarke I.N.,
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:114-19(1997).
DR EMBL, Z19927, CAAG820911;
DE InterPro: IPR004006; Calici_coat
DE Pfam: PF00915; Calici_coat; 1
FT NON_TER 1
FT NON_TER 58
FT NON_TER 58
SQ SEQUENCE 58 AA; 4086 MW; CA9A7C193R9CQ02D CRC64;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best local similarity 100.0%; Pred No 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 50 VLEP 53

RESULT 11
O39632 PRELIMINARY; FET; 19 AA.
ID O39632;
AC O39632;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Capsid protein (Fragment).
OS Calicivirus.
CC Virus; ssRNA positive strand viruses; no DNA stage; Caliciviridae
CX NCBI_TaxID=11975;
RN [1]_TaxID=11975;
FC SEQUENCE FROM N.A.
RC STRAIN-CAPMAFTHN/94/UX.
RA MEDLINE=97279118, PubMed=9131452,
RX Green S.M., Lambden P.R., Owen G.A., Clarke I.N.,
RT "Capsid sequence diversity in small round structured viruses from
RT recent UK outbreaks of gastroenteritis.";
RL J. Med. Virol. 52:114-19(1997).
DR EMBL, Z19927, CAAG820911;
DE InterPro: IPR004005; Calici_coat.
DE Pfam: PF00915; Calici_coat; 1.
FT NON_TER 1
FT NON_TER 58
FT NON_TER 58
SQ SEQUENCE 58 AA; 4097 MW; A3PF42CF412441D CFC04;

Query Match 100.0%; Score 20; DB 12; Length 58;
Best local similarity 100.0%; Pred No 5.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 50 VLEP 53

RESULT 12
O55728 PRELIMINARY; FET; 61 AA.
ID O55728;
AC O55728;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical 7.4 kDa protein.
OS Chilo iridescent virus (CIV) (Insect iridescent virus type 6).
CC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
CX NCBI_TaxID=10498;
RN [1]_TaxID=10498;
FC SEQUENCE FROM N.A.

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RA Bahr U., Tidona C.A., Darai G.;
RL Virus Genes 0:0-0(1997).
DR EMBL: AF303741; AAR04439 1; -.
RW Hypothetical protein.
SQ SEQUENCE 61 AA; 7395 MW; AF71PA75RC14AE0A CRC64;

Query Match 100.0%; Score 20; DB 12; Length 61;
Best local similarity 100.0%; Pred No 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 53 VLEP 56

RESULT 13
Q97US6 PRELIMINARY; PPT; 62 AA.
ID Q97US6;
AC Q97US6;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Second OPP in transposon ISC1058.
GN SSO11456.
OS Sulfolobus solfataricus.
CC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
CX MFP: T3x12-2287;
RN [1]_TaxID=2287;
FC SEQUENCE FROM N.A.
RC STRAIN-ATCC 35092 / DSM 1617 / P2;
FX MEDLINE=97279118, PubMed=9131452,
RX Ste G., Singh P.K., Confalonieri P., Sivaprasad V., Allard G.,
PA Aways M.J., Chan-Waiher C.C.-Y., Clausen I.G., Curtis B.A.,
PA De Meers A., Brause G., Fletcher G., Gordon P.V.K.,
PA Heikamp-de Jung W., Jeffries A.C., Kozak G.L., Medina N., Peng X.,
PA Thi-Ngoc H.P., Redder P., Schenck W.E., Thariani C., Palstrup N.,
PA Charlebois P.L., Doolittle W.F., Duguet M., Gaasterland T.,
PA Carter P.A., Pugh M.A., Seibert G.W., Van der West J.,
PT "The complete genome of the crenarchaeon Sulfolobus solfataricus P2."
RC Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR EMRL; A0066881; AAK41026 1; -.
RW Complete Proteome.
SQ SEQUENCE 62 AA; 6561 MW; C0CBEBPBI3P43PF CPO64;

Query Match 100.0%; Score 20; DB 17; Length 62;
Best local similarity 100.0%; Pred No 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 20 VLEP 23

RESULT 14
Q9FEX8 PRELIMINARY; PPT; 63 AA.
ID Q9FEX8;
AC Q9FEX8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Putative lectin (Fragment).
GN HL2.
OS Hordeum vulgare (Barley).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
CC Triticaceae; Hordeum.
CX NCBI_TaxID=4513;
RN [1]_TaxID=4513;
FC SEQUENCE FROM N.A.
RC TISSUE-ETIOLOGED COLEOPTILE;
DE Klopstech K.R.;
RA Klopstech K.R.;
RW Submitted (01-03-2000) to the EMBL/GenBank/CCP databases.

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=ETIOLOGATED COLLEOPTILE;
RA  Grunwald I.;
RL  Thesis (2001), Department of Biological Sciences,
RG  University of Hannover, Hannover, Germany.
DR  EMBL; AC030112; CAC19669.1;
KW  Lectin.
FT  NON_TER 1 63
FT  NON_TER 63 63
SQ  SEQUENCE 63 AA; 6948 MW; D794D32B1A5A8C93 CRQ64;

Query Match 100.0%; Score 20; DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 54 VLEP 57

RESULT 15
Q99WL3 PRELIMINARY; PRT; 63 AA.
AC Q99WL3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein SAV0364
GN SAV0364 OP SAV0361 OP SAS009
OS Staphylococcus aureus (strain M50 / ATCC 26958), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]_TaxID=158878, 158879;
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain M50), and S.aureus (strain N315);
RX MEDLINE=2111952, PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Ouchi A., Aoki K.-I., Nagai Y., Imai Y.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue P.-I., Fatio C.,
RA Sekimizu K., Hirakawa H., Fuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1243(2001)
DR EMBL; AF003359; BAB56526.1;
DR EMBL; AF003130; BAB41576.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 63 AA; 7061 MW; 4B06A9A5A56A96C4 CRQ64;

Query Match 100.0%; Score 20; DB 16; Length 63;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 35 VLEP 38

RESULT 16
Q05120 PRELIMINARY; PRT; 64 AA.
AC Q05120;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to a putative ccf in the m3pS region of Rhodobacter
DE sphaeroides (Fragment)
OS Methylobacterium extorquens.

OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Methylobacterium group; Methylobacterium.
OX NCBI_TaxID=408;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AM1;
RX MEDLINE=97386438; PubMed=9244287;
RA Chistoserdova L., Lidstrom M.E.;
RT "Identification and mutation of a gene required for glycerate kinase
RT activity from a facultative methylotroph, Methylobacterium extorquens
RT AM1.";
RL J. Bacteriol. 179:4946-4948(1997).
RF EMBL; Y87316; AAE66500.1;
DR InterPro; IPR001449; TPR.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 64 AA; 7417 MW; F28A40CC4D121E7F CRQ64;

Query Match 100.0%; Score 20; DB 2; Length 64;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 6 VLEP 9

RESULT 17
Q14390 PRELIMINARY; PRT; 65 AA.
AC Q14390;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 7.4 kDa protein (Fragment).
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC NCBI_TaxID=4896;
RN [1]_TaxID=4896;
RP SEQUENCE FROM N.A.
RC STRAIN=972H;
RA Jiang Y.-J., Yoo H.-S.;
PL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97376; AAB63868.1;
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 65
SQ SEQUENCE 65 AA; 7163 MW; 553F55F67E34824 CRQ64;

Query Match 100.0%; Score 20; DB 3; Length 65;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 29 VLEP 32

RESULT 18
Q92QK7 PRELIMINARY; PRT; 68 AA.
AC Q92QK7;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ATG07350 protein.
GN ATG07350.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicot; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

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BN SEQUENCE FROM N.A.
 PP STRAIN-CV_ COLOMBIA;
 RX MELLINE-25033497; PubMed:13617197;
 RA Lin X., Kaul S., Pounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.F., Feldblum T.V.,
 RA Puell C.P., Ketchum K.A., Lee J.J., Panning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Unayam L., Tallon L.J., Gill J.E.,
 RA Adams W.D., Collins A.J., Tinsley T.H., Gordon H.M., Somerville C.S.,
 RA Copenhaver G.P., Preuss D., Vierman W.C., White G., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana";
 RL Nature 402:761-768 (1999).
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV_ COLOMBIA;
 RA Lin X.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DP EMBL; AC004217; AAC15527.1;
 SQ SEQUENCE 68 AA; 7727 MW; 6A67C97F8999FDCE0 CRC64;

Query Match 100.0%; Score 20; DB 10; Length 68;
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 6 VLEP 9
 RESULT 19
 ID Q90M7 PRELIMINARY; PPT; 71 AA.
 AC Q90M7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Agouti-related protein (fragment).
 OS Coturnix coturnix japonica (Japanese Quail)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Coturnix;
 CX NCBI_TaxID:93934;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-HYPOTHALAMUS;
 RA Buswell T., Li Q., Takeuchi S.;
 RT "Neurons expressing neuropeptide Y mRNA in the infundibular
 hypothalamus of Japanese Quail are activated by fasting and co-express
 Agouti-related protein mRNA";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY048849; AAL06600.1;
 FT NON-TER
 SQ SEQUENCE 71 AA; 7826 MW; EF0412E7A71B22 CRC64;

Query Match 100.0%; Score 20; DB 13; Length 71;
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 3 VLEP 6
 RESULT 20
 ID Q9UJ82 PRELIMINARY; PPT; 74 AA.
 AC Q9UJ82;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Brain cDNA clone MNCB-2875.

GN A030009H04PIK
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A
 RC STRAIN=C57BL;
 RA Osada N., Kusuda J., Tanuma P., Ito A., Hirata M., Sugano S.,
 RA Hashimoto K.;
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library
 made by oligo-capping method";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB041807; BAA35115.1;
 DP MGD; MGI:1915159; A030009H04PIK
 SQ SEQUENCE 74 AA; 8117 MW; 606971B6026B5E99 CRC64;

Query Match 100.0%; Score 20; DB 11; Length 74;
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 42 VLEP 45
 RESULT 21
 ID Q99Q00 PRELIMINARY; PPT; 77 AA.
 AC Q99Q00;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical protein SCPI.332.
 GN SCPI.332 ANP SCPI.22c
 OS Streptomyces coelicolor
 OG Plasmid SCPI.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomyces;
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A
 RC STRAIN=A3(2);
 RA Bentley S.D., Chirer K.P., Cardeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.P., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Hafter D., Pateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornby T., Howarth S.,
 RA Huang C.H., Kieser T., Larke T., Murphy L., Oliver K., O'Neill S.,
 RA Rabinovitch E., Rajandream M.A., Rutherford K., Buxter S.,
 RA Seeger F., Saunders D., Sharp S., Squares P., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrall R.G., Parkhill J.,
 RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2)";
 RL Nature 417:141-147 (2002)
 DP EMBL; AL500464; CAC36857.1;
 CP EVG2; AK00467; CAC36544.1;
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 77 AA; 8145 MW; 69E94CE92E234F08 CRC64;

Query Match 100.0%; Score 20; DB 16; Length 77;
 Best Local Similarity 100.0%; Pred. No. 6 aa+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 71 VLEP 74
 RESULT 22
 ID Q9VEI3 PRELIMINARY; PPT; 77 AA.
 AC Q9VEI3;

```

DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein APE5025.
GN APE5025.
OS Aetopyrum pernix.
OC Archaea: Crenarchaeota: Thermoterrae: Desulfurococcales;
OC Desulfurococaceae; Aetopyrum
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=98310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Hatikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaï A., Kosugi H.,
RA Haseyama A., Fukui S., Naito Y., Nishitani K., Nakarawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
RA Yamazaki J., Kushida N., Omori A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aetopyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL: AF000600; HAA70563.1; -
FW Hypothetical protein, complete protein.
SQ SEQUENCE // AA: 4700 MW: 426100 PEPASQ CP64;

Query Match 100.0%; Score 20; DB 17; Length 77;
Best Local Similarity 100.0%; Pred. No. 6 Refs;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 10 VLEP 33

RESULT 23
P97585
ID P97585 PRELIMINARY; PPT; 79 AA.
AC P97585;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 09, Last annotation update)
DE Dihydroethione-inducible gene-2 (Fragment).
GN DIG-2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Petrus
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FISHER 344;
RX MEDLINE=9712421; PubMed=868041;
RA Primiano T., Gastel J.A., Kensler T.W., Surter T.P.;
RT "Isolation of cDNAs representing dihydroethione responsive genes.";
PL Carcinogenesis 17:2297-2303(1996).
DR EMBL: U66323; AAB3982.1; -
FT NON TER 79
SQ SEQUENCE 79 AA; 7999 MW; F45B17AFFA7390AF CRC64;

Query Match 100.0%; Score 20; DB 11; Length 39;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 5 VLEP 8

RESULT 24
Q01970
ID Q01970 PRELIMINARY; PPT; 80 AA.
AC Q01970;
DT 01-JUL-1997 (TREMBlrel. 04, Created)

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DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 9.5 kDa protein.
GN M01D7.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;
OC Phaditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
PL Science 282:2012-2018(1998)
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
PA Gattung S., Goela D.;
RT "The sequence of C. elegans cosmid M01D7.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
PA Waterston R.;
RT "Direct Submission.";
EL Submitted (AUG 2001) to the EMBL/GenBank/DBJ databases.
DP EMBL: AF003739; AAE58066.1; -
KW Hypothetical protein.
SQ SEQUENCE 80 AA; 9457 MW; 70889FB8AAF87D0C CRC64;

Query Match 100.0%; Score 20; DB 5; Length 80;
Best Local Similarity 100.0%; Pred. No. 7 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 72 VLEP 75

RESULT 25
Q9Q086
ID Q9Q086 PRELIMINARY; PPT; 81 AA.
AC Q9Q086;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RA Fickel J., Czupalla O.;
RT "Canine distemper virus in a fox (Vulpes vulpes)";
PL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF158979; AAB47562.1; -
DR InterPro: IPR000776; Fusion.gly.
DE Flam, PF09523, Fusion.gly. 1.
FT NON TER 81
SQ SEQUENCE 81 AA; 8768 MW; 7791FF09B40DEB6B CRC64;

Query Match 100.0%; Score 20; DB 12; Length 81;
Best Local Similarity 100.0%; Pred. No. 7 1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 36 VLEP 39

```

Search completed: March 5, 2003, 08:33:22
Job time : 32 secs

XX Ashkar S;
 XX WPI: 2000-687159/67
 XX New osteopontin-derived chemotactic and inhibitory peptides, useful for
 PT promoting scarless wound healing, modulating cellular chemotaxis,
 PT treating formation of atherosclerotic plaques and preventing metastasis
 XX
 XX Claim 14; Page 42; 54pp; English.
 XX The present sequence is an osteopontin-derived chemotactic peptide.
 CC Such chemotactic peptides are useful for promoting scarless wound
 CC healing, modulating chemotaxis and promoting cell migration to a target
 CC site in a cell of a subject. They are also used for modulating cellular
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
 CC useful for treating the formation of atherosclerotic plaques in a
 CC subject. The peptides are used for preventing metastasis, treating an
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
 CC tumour metastasis or ocular neovascularisation. They are also used for
 CC activating cell apoptosis, for modulating nitrous oxide production and
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune
 CC diseases. They can also be used to enhance an immune response by
 CC attracting macrophages
 XX
 XX Sequence 6 AA;
 Query Match 100.0%; Score 20; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 DB 2 VLEP 5
 RESULT 4
 AAW06132
 ID AAW06132; standard; Peptide; 8 AA
 XX
 AC AAW06132;
 XX
 DT 17-JAN-1997 (first entry)
 XX
 DE N-terminus of receptor-type tyrosine kinase protein ligand
 XX
 KW Receptor type tyrosine kinase; ligand; Comma staining, PAS staining,
 KW N-terminus; human.
 XX Homo sapiens.
 XX JP08188596-A.
 XX 23-JUL-1996.
 XX 13-JAN 1995; 94JP 0003677.
 XX 09-NOV-1994; 94JP 0275411.
 PR 19-OCT-1994; 94JP 023484A
 XX (ASAH) ASAH1 FASEI K00Y0 YV
 XX WPI: 1996-388601/39.
 XX New ligand for receptor type tyrosine kinase - has mol.wt. 22-25
 PT kilodalton(s) and is positive for Comma staining and PAS staining
 XX Claim 3; Page 43; 51pp; Japanese.
 XX This sequence represents the N-terminus of a receptor-type tyrosine

CC kinase receptor binding ligand of the invention (see AAW06133) and
 CC AAW06134). The ligands of the invention recognise the fragment of the
 CC receptor type kinase receptor represented by AAW06130 (see AAW06131 for
 CC full length sequence). The proteins of the invention have a molecular
 CC weight of 23500 (plus or minus 1500) Da, and are positive for Comma stain
 CC staining and PAS staining. The protein is a new ligand of receptor type
 CC tyrosine kinases, and can be prepared by standard recombinant
 CC techniques.
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 20; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 DB 4 VLEP 7
 RESULT 5
 AAR94654
 ID AAR94654; standard; Protein; 8 AA.
 XX
 AC AAR94654;
 XX
 DT 18 OCT-1996 (first entry)
 XX
 DE Fragment of receptor type tyrosine kinase (TK) ligand.
 XX
 KW Receptor type tyrosine kinase, TK, ligand; differentiation;
 KW haematopoietic stem cell; tyrosine; bone marrow; leukaemia.
 XX Homo sapiens.
 XX W09611212-A1.
 XX 18-APR-1996.
 XX 09-OCT-1995; 95WO-JP02069.
 XX 22-DEC-1994; 94JP 0320712.
 PR 07-OCT-1994; 94JP 0244433.
 PR 20-OCT-1994; 94JP 0302882.
 XX (ASAH) ASAH1 FASEI K00Y0 YK.
 XX Ohno M, Sakano S;
 XX WPI: 1996-209809/21.
 XX Ligand peptide binding to receptor-type tyrosine kinase - enhances
 PT intracellular tyrosine phosphorylation, useful for investigation of
 PT undifferentiated blood cell behaviour
 XX
 XX Disclosure; Page 162; 193pp; Japanese.
 XX A ligand polypeptide which binds to the extracellular part of a
 CC specific receptor-type tyrosine kinase and induces phosphorylation
 CC of tyrosine within the cell can be used in the study of the
 CC differentiation of blood cells such as the haematopoietic stem
 CC cells, of disease processes such as leukaemia, and of the biology of
 CC bone marrow transplantation. The ligand plays a role in the
 CC differentiation process and the specific ligand target is expressed
 CC in undifferentiated blood cells.
 XX
 XX Sequence 8 AA;
 Query Match 100.0%; Score 20; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4

DB 4 VLEP 7
 ||||
 Best Local Similarity 100.0%; Pred. No 7 aa-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 AAR84629
 ID AAR84629 standard; Peptide; 9 AA.
 XX
 AC AAR84629;
 XX
 DT 02-JUN-1996 (first entry)
 XX
 DE Wheat acetyl-Coenzyme-A-carboxylase peptide sequence.
 XX
 KW Acetyl Coenzyme A carboxylase; ACCase; plasmid pK11;
 KW transgenic plant, modified oil content;
 KW polyhydroxyalkanoate polymer; herbicide resistance;
 KW monodact crop improvement
 OS
 XX Triticum aestivum.
 XX
 PN WC9529246-A1.
 XX
 PD 02-NOV-1995.
 XX
 PF 21-APR-1994; 94WO-GB00846.
 XX
 PR 21-APR-1994; 94WO-GB00846.
 XX
 PA (ZENE) ZENECA LTD.
 XX
 PI Bright SWJ, Elborough KM, Pentem PA, Glasas AP;
 XX
 DR WPI; 1995 192004/49
 XX
 XX DNA encoding acetyl Coenzyme A carboxylase - used for developing
 PT plants with controlled expression of ACCase, e.g for controlling
 PT fatty acid synthesis.
 XX
 PS Disclosure; Fig 3; 61pp; English.
 XX
 CC Wheat acetyl Coenzyme A carboxylase (ACCase) was partially
 CC purified from wheat germ and a dominant 220 kDa band was identified
 CC as ACCase by column chromatography and SDS-PAGE. After
 CC purification in the gel, the protein was hydrolysed using
 CC endoproteinase LysC, and resulting peptides were purified by
 CC electrophoresis and loaded onto an Axi 477A pulse fixed
 CC protein sequencer. Sequence data of 4 peptides (this peptide and
 CC peptides AAR84625, AAR84627 and AAR84631) were compared with plasmid
 CC pK11-derived amino acid sequences (AAR84630, AAR84636, AAR84638 and
 CC AAR84632) so as to authenticate pK11 (see AAT04948) as wheat ACCase
 CC cDNA. More specifically, this peptide corresponds to
 CC amino acids 419-437 of the pK11 deduced AA sequence AAR84619,
 CC (i.e. AAR84630). Partial cDNA clone pK11 (NCIB 40553) can be
 CC used to create a sense/antisense expression cassette to
 CC transform rape and other oilseed plants (canola, soybean,
 CC sunflower) to downregulate production of the ACCase enzyme.
 CC The transgenic plants have a lower or a modified oil content.
 CC Down-regulation of oil synthesis can be used to divert the
 CC substrate, acetyl Coenzyme A, into synthesis of alternative
 CC storage materials (starch, protein or novel polymers e.g.
 CC polyhydroxyalkanoates). Full-length ACCase clones can be used
 CC to create transgenic plants over-expressing ACCase, and
 CC therefore with increased oil content. ACCase over-expression in
 CC wheat plants such as wheat, barley, maize and rice, which are
 CC normally sensitive to herbicides, results in
 CC aryloxyphenoxy-friginate and alkylketone herbicide resistance in
 CC the transgenic plants (dicots are normally resistant to these
 CC herbicides).
 XX
 SQ Sequence 9 AA.

Query Match 100.0%; Score 20; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred No 9;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 AAY07169
 ID AAY07169 standard; Peptide; 10 AA.
 XX
 AC AAY07169;
 XX
 DT 02-JUN-1999 (first entry)
 XX
 DE HLA binding peptide.
 XX
 KW Cancer associated antigen; diagnosis; research; treatment; human;
 KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
 KW prostate cancer.
 XX
 OS Homo sapiens.
 XX
 PN WC9904265-A2.
 XX
 PD 28-JAN-1999.
 XX
 PF 15-JUL-1998; 98WO-US14679.
 XX
 PR 22-JUN-1999; 98US 0102222.
 XX
 PP 17-JUL-1997; 97US-0896164.
 XX
 PP 10-OCT-1997; 97US-0061539.
 XX
 PP 10-OCT-1997; 97US-0061765.
 XX
 PP 10-OCT-1997; 97US-0948705.
 XX
 PP 11-OCT-1997; 97GR-0021697.
 XX
 PA (LUDWIG) LUDWIG INST CANCER RES.
 XX
 PI Chen Y, Gout I, Gure A, O'Hare M, Ohta Y, Old LJ;
 PI Pfeundschoh M, Sahin U, Scanlan MJ, Stockert E;
 PI Tureci O;
 XX
 DR WPI; 1999-132448/11.
 XX
 PT New isolated cancer associated nucleic acids and polypeptides -
 PT isolated using sera from cancer patients, used to develop products
 PT for the diagnosis, monitoring or treatment of cancers
 XX
 PS Example 16; Page 762; 787pp; English
 XX
 CC The invention relates to a method for diagnosing a disorder characterised
 CC by expression of a human cancer associated antigen precursor coded for by
 CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
 CC biological sample isolated from a subject with an agent that specifically
 CC binds to the NAM, an expression product or a fragment of an expression
 CC product complexed with an RNA molecule; and (b) determining the
 CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 20; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred No 20;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 ||||
 Best Local Similarity 100.0%; Pred No 4;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 VLEP 8
||||

RESULT 8

AAV07127
ID AAY07127 standard; Peptide; 10 AA.

XX AC AAY07127;
XX DE 02-JUL-1999 (first entry)
XX DE HLA binding peptide.
XX KW Cancer associated antigen, diagnosis, research, treatment; human;
XX KW breast cancer; colon cancer; gastric cancer; local cancer; lung cancer;
XX KW prostate cancer.
XX OS Homo sapiens.
XX PN W09904265-A2.
XX PD 28 JAN-1999.
XX PF 15-JUL-1998; 98WO-US14679.
XX PR 22 JUN 1998; 98US 0102322.
XX PR 17-JUL-1997; 97US-006164.
XX PR 10-OCT-1997; 97US-0061599.
XX PR 10-OCT-1997; 97US-0061765.
XX PR 10-OCT-1997; 97US-0948705.
XX PR 11 OCT-1997; 97US-0061597.
XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI Chen Y, Gout I, Gatt A, G'Hare M, Ghata Y, Old LJ;
XX PI Pfeleuschuh M, Sahin U, Scanlan MJ, Stockert F;
XX PI Tureci O;
XX DR WPI; 1999-132448/11.
XX PT New isolated cancer associated nucleic acids and polypeptides;
XX PT isolated using sera from cancer patients, used to develop products
XX PT for the diagnosis, monitoring or treatment of cancers
XX PS Example 16; Page 765; 787pp; English.
XX CC The invention relates to a method for diagnosing a disorder characterised
XX CC by expression of a human cancer associated antigen precursor coded for by
XX CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX CC biological sample isolated from a subject with an agent that specifically
XX CC binds to the NAM, an expression product or a fragment of an expression
XX CC product complexed with an HLA molecule; and (b) determining the
XX CC interaction between the agent and the NAM or the expression product as a
XX CC determination of the disorder. The products and methods can be used in
XX CC the diagnosis, monitoring, research, or treatment of conditions
XX CC characterised by the expression of various cancer associated antigens.
XX CC The invention provides nucleic acid sequences and encoded polypeptides
XX CC which are cancer associated antigen precursors expressed in human breast
XX CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX CC lung cancer.

XX SQ Sequence 10 AA;

Query Match 100 %; Score 20; PR 20; Length 10;
Best Local Similarity 100 %; Pled No 90;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
||||
Db 5 VLEP 8

RESULT 9

AAW00583
ID AAW00583 standard; Peptide; 14 AA.

XX AC AAW00583;
XX DT 01-OCT-2001 (first entry)
XX DE Human transcription factor fragment SEQ ID NO: 1131.
XX DE Human, single nucleotide polymorphism, SNP, paternity test;
XX KW forensic test; aberrant protein expression.
XX OS Homo sapiens.
XX PR W000000000-A2
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US00322.
XX PR 07-JAN 2000; 2000US 0174962.
XX PA (CURA-) CURAGEN CORP.
XX PI Shimkets RA, Leach MD;
XX DR WPI; 2001-451871/48.
XX DR N-PSDB; AAH89700.
XX PT Isolated human polynucleotides containing single nucleotide
XX PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
XX PT infection and diabetes

XX PS Disclosure; Page 427; 475pp; English.

XX CC The present invention relates to human nucleic acids containing single
XX CC nucleotide polymorphisms (SNPs). These can be used in forensic and
XX CC paternity tests, and to aid in the treatment of diseases associated with
XX CC aberrant protein expression, including cancer, amyloidosis, diabetes,
XX CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
XX CC glomerulonephritis, haemolytic anaemia, thrombocytopaenia, arthritis,
XX CC meningitis, muscular disorders, dementia, neurological diseases, infectious
XX CC scrofula, male infertility, hypercalcaemia, blood pressure disorders,
XX CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
XX CC autoimmunity. The present sequence is a peptide encoded by a
XX CC polymorphism-containing oligonucleotide fragment of the invention.

XX SQ Sequence 14 AA,

Query Match 100 %; Score 20; PR 20; Length 14;
Best Local Similarity 100 %; Pled No 13602;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
||||
Db 5 VLEP 8

RESULT 10

AAB08085
ID AAB08085 standard; peptide; 17 AA.

XX AC AAB08085;
XX DT 24 DEC-2000 (first entry)
XX DE Amino acid sequence of a helper T cell epitope from CDV.
XX KW T helper cell epitope; CDV; immune response; Canine vaccine.
XX OS Canine distemper virus.

```

PN WC200046390-A1.
XX
PD 10-AUG-2000.
XX
XX 07-FEB-2000; 2000WQ-AU000070
XX
XX 05-FEB-1999; 99AU-0008533.
XX 04-AUG-1999; 99AU-0002013.
XX
XX (UYME ) UNIV MELBOURNE.
XX (CSIC-) CSL LTD.
XX (CSIP ) COMMONWEALTH SCI & IND RES ORG.
XX (CCON ) COUNCIL QUEENSLAND INST MEDICAL RES.
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX
XX Jackson DC, Souravi G, Walker J;
PI
XX
XX WPI, 2000-532904/48.
XX
XX Novel T helper cell epitopes derived from canine distemper virus useful
PT for preparation of canine vaccines -
XX
XX Claim 1, Page 28; 54pp; English.
XX
XX AAB08076-B08101 represent T helper cell epitopes, derived from canine
CC distemper virus (CDV). Compositions comprising these T cell helper
CC epitopes are useful for inducing an immune response in an animal. The
CC epitopes are useful as components of animal, in particular, canine
CC vaccines, either simply as synthetic peptide based vaccines and as
CC additions to vaccines containing more complex antigens.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 20; DB 21; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLEP 4
DB 6 VLEP 9
RESULT 12
AAW70175
ID AAW70175 standard; peptide; 19 AA.
XX
XX AAW70175;
XX
XX 07-DEC-1998 (first entry)
XX
XX Internal peptide fragment of CFP 9.
XX
XX Culture filtrate protein; CFP, H37RV, 2-D PAGE, electrophoretic, trypsin;
XX C18 capillary reversed phase chromatography; Heterology; antigen; antibody;
XX human immunodeficiency virus; HIV.
XX
XX Mycobacterium tuberculosis.
XX
XX WO9829132-A1.
XX
XX 09-JUL-1998.
XX
XX 29-DEC-1997; 97WQ-US24189.
XX
XX 31-DEC-1995; 94US-0034003
XX (UYNY ) UNIV NEW YORK STATE.
XX
XX Belisle JT, Laal S, Zolla-Pazner S,
XX
XX WPI; 1998-187787/13
XX
XX Early detection of mycobacterial infection - by testing a biological
XX fluid sample from a subject for the presence of anti-CD4 reactive
XX with Mycobacterium tuberculosis antigens
XX
XX Example 5; Page 88; 170pp; English.
XX
XX Sequences AAW70167-W70179 are internal peptide fragments of selected
XX culture filtrate proteins (CFPs) of M. tuberculosis (Mt), strain H37RV,
XX determined by LC MS-MS analysis. To obtain these sequences, the
XX proteins were resolved by 2-D PAGE, transferred to a membrane by
XX electroblotting, stained, destained, subjected to in-gel proteolytic
XX digestion with trypsin, and then eluted and separated by C18 capillary
XX reversed phase chromatography. These antigens and antibodies that form
XX against them can be used for the early detection of mycobacterial
XX disease, particularly in subjects infected with human immunodeficiency
XX virus (HIV).
XX
XX Sequence 19 AA;
SQ

```

Query Match 100.0%; Score 20; PR 19; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 DB 15 VLEP 18

RESULT 13
 ID AAE05631 standard; peptide; 19 AA.
 AC AAE05631;
 XX 24-SEP-2001 (first entry)
 DE Internal peptide fragment #9 of Mycobacterium tuberculosis protein IT-42.
 KW Mycobacterial disease; infection; 88 kDa protein; tuberculosis; TP;
 KW liquid chromatography-mass spectrometry-mass spectrometry; LC-MS-MS;
 KW culture filtrate protein; GFP; H37Rv; early antigen; serodiagnosis;
 KW human immunodeficiency virus; HIV; protein IT 42.
 XX Mycobacterium tuberculosis.
 OS US6245331-B1.
 PN 12-JUN-2001.
 PD 31-DEC-1997; 97US-0001984.
 PR 02-JAN-1997; 97US-0034003.
 PA (UNIV-) UNIV NEW YORK MEDICAL CENT.
 PA (COLS) UNIV COLORADO STATE.
 PI Laal S, Zolla-Pazner S, Belisle JT;
 XX WPI; 2001-424324/45.

DR Detecting a mycobacterial disease (tuberculosis) in individuals
 PT comprise assaying a biological sample for the presence of
 PT anti-Mycobacterium tuberculosis antibodies or M. tuberculosis
 PT antigen-antibody complex
 XX Example 5, Column 55-56; 96pp; English.
 CC The present invention relates to a method for early detection of active
 CC mycobacterial disease or infection comprises assaying a biological fluid
 CC sample for the presence of early antibodies specific for an 88-kDa
 CC Mycobacterium tuberculosis (Mt) protein or immune complexes consisting of
 CC an 88-kDa M. tuberculosis protein antigen complexed with an antibody
 CC specific for the antigen. The method is useful for the early and rapid
 CC detection of mycobacterial disease, particularly tuberculosis, in
 CC individuals at heightened risk of developing tuberculosis. This
 CC individuals include human immunodeficiency virus (HIV)-infected subjects
 CC or other immunocompromised individuals. The method is a rapid and
 CC inexpensive screening procedure for detecting mycobacterial disease.
 CC The present sequence is an internal peptide fragment of M. tuberculosis
 CC protein IT-42. The N-terminal peptide or internal peptide fragment is
 CC identified by liquid chromatography-mass spectrometry-mass spectrometry
 CC (LC-MS-MS) of selected Mt culture filtrate proteins (CFPs) of Mt H37Rv
 CC early antigen, used in the exemplification of the invention. The H37Rv
 CC early antigen is used in the serodiagnosis of tuberculosis (TB).
 XX Sequence 19 AA;

Query Match 100.0%; Score 20; PR 22; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 DB 15 VLEP 18

RESULT 14
 ID AAB50346 standard; peptide; 20 AA.
 AC AAB50346;
 XX 09-MAR-2001 (first entry)
 DE Adeno-associated virus capsid immunogenic peptide #4.
 KW Adeno-associated virus; AAV; capsid; virus binding inhibition;
 KW competitive inhibitor; immunogen; epitope.
 XX Mastadenovirus.
 OS W01067331F A2
 XX 07 DEC 2000.
 PD 20-MAY-2000; 2000WO-US14466
 PP 28-MAY-1999; 99US-0321589.
 XX (CELL-) CELL GENESYS INC.
 PI Patel S, McArthur J;
 XX WPI; 2001-061507/07
 DE New polypeptide portion of a virus protein binding to an antibody
 PT specific for the virus useful for inhibiting binding of the virus to a
 PT cell or for binding host antibody to provide a transient tolerant or
 PT non-responsive state
 XX Disclosure; Fig 4; 33pp; English.

CC The present sequence is given in a specification relating to
 CC polypeptide portions of a virus protein or its derivative, that bind to
 CC an antibody specific for the virus or inhibit binding of the virus to a
 CC cell. The polypeptides are used in inhibiting the binding of viruses to
 CC cells of a host. Oligopeptides that inhibit binding of virus to
 CC receptor can be used as competitive inhibitors to release bound virus
 CC in an adsorption-type assay, and if an antibody was used as an
 CC immunoadsorbent, the oligopeptide could be used to elute bound virus
 CC from a solid support to which virus antibody is immobilized. These
 CC oligopeptides may further be used to bind to host antibody to provide a
 CC transient tolerant or non-responsive state.

SQ Sequence 20 AA;

Query Match 100.0%; Score 20; PR 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 DB 13 VLEP 16

RESULT 15
 ID AAR79207 standard; peptide; 25 AA.
 AC AAR79207;
 XX 06-MAR-1996 (first entry)
 DE TGF-beta5 residues 358-382.

```

XX Chemotactic, transforming growth factor-beta, TGF-beta, fibroblast,
KW inflammatory cell, neurophil, monocyte, macrophage, proliferation,
KW collagen synthesis; wound healing
XX
XX Homo sapiens.
XX
XX US5436228-A.
XX
XX PD 25-JUL-1995.
XX
XX PF 12 DEC 1995. 90US-0626631
XX
XX PR 24-SEP-1993. 90US-0127909
XX
XX PR 12-DEC-1990. 90US-0626631.
XX
XX (KANG/) KANG A.
PA (POST/) POSTLETHWAITE A E.
PA (SEVE/) SEYER J.
XX
XX Kang A, Postlethwaite AE, Seyer J;
XX
XX WPI; 1995-269831/35
XX
XX Novel chemotactic peptide(s) based on transforming growth
PT factor-beta - used to induce chemotaxis and proliferation of
PT fibroblasts and inflammatory cells, partic. for wound healing
XX
XX Claim 5; Column 8; 28pp; English
XX
XX The sequences given in AAP79188-207 are chemotactic peptides derived
CC from four overlapping regions of transforming growth factor (TGF)-beta
CC isoforms 1-5. These peptide correspond to the regions 368-374, 364-378,
CC 365-387 and 358-392 from the carboxy terminal portion of the TGF-beta
CC isoforms. The numbering of the positions of the peptides is based on
CC TGF-beta1. These peptides possess chemottractant properties for
CC fibroblasts and inflammatory cells, including neutrophils and
CC monocytes/macrophages. They also stimulate fibroblast proliferation
CC and collagen synthesis. They are partic. used to promote wound
CC healing.
XX
XX Sequence 25 AA;
XX
XX Query Match 100.0%; Score 20; DB 16; Length 25;
XX Best Local Similarity 100.0%; Pred No. 2 4e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX ||||
XX Db 4 VLEP 7
XX
XX RESULT 16
XX AAW67273
XX ID AAW67273 standard; peptide; 25 AA.
XX
XX AC AAW67273;
XX
XX DT 21 DEC 1998 (first entry)
XX
XX DE Peptide #20 with chemotactic activity.
XX
XX Chemotactic activity; wound healing; transforming growth factor;
KW chemotaxis, fibroblast, collagen synthesis.
XX
XX Synthetic.
XX
XX OS Homo sapiens.
XX
XX PN US5824647-A.
XX
XX PD 20-OCT-1998.
XX
XX PF 12-DEC-1990. 90US-0626631.
XX

```

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XX 01-JUN-1995. 90US-0457353.
XX
XX 12-DEC-1990. 90US-0626631.
XX
XX 29 SEP-1993. 90US-0127909.
XX
XX (KANG/) KANG A.
PA (POST/) POSTLETHWAITE A E.
PA (SEVE/) SEYER J.
XX
XX Kang A, Postlethwaite AE, Seyer J;
XX
XX WPI; 1999-090507/40
XX
XX Chemotactic peptide(s) for e.g. wound healing - corresponding to
PT fragments of transforming growth factor beta isoforms
XX
XX Disclosure; Column 4; 34pp; English.
XX
XX The invention relates to chemotactic peptides which are used for inducing
CC chemotaxis of fibroblasts and/or inflammatory cells in vitro or in vivo;
CC for inducing proliferation of fibroblasts and/or inflammatory cells in
CC vitro or in vivo; for inducing collagen synthesis by fibroblasts in vitro
CC or in vivo; and for promoting wound healing. The present sequence
CC represents a chemotactic peptide disclosed in the specification.
XX
XX Sequence 25 AA;
XX
XX Query Match 100.0%; Score 20; DB 19; Length 25;
XX Best Local Similarity 100.0%; Pred No. 2 4e+02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 VLEP 4
XX ||||
XX Db 4 VLEP 7
XX
XX RESULT 17
XX AAR52310
XX ID AAR52310 standard; peptide; 26 AA.
XX
XX AC AAR52310;
XX
XX DT 30-SEP-1996 (first entry)
XX
XX DE Mouse heavy chain surface patch MUSTIGHWN.
XX
XX antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.
XX
XX OS Mus sp.
XX
XX PN EP592106-A1.
XX
XX PD 13-APR-1994.
XX
XX PF 07-SEP-1993. 93EP-0307051.
XX
XX PR 09 SEP-1992. 90US-0942245.
XX
XX (PEDP/) PEDERSEN J T.
PA (IMM/) IMMUNOGEN INC.
XX
XX Guild BC, Pedersen JT, Pees AP, Poguska MA, Searle SMJ;
XX
XX WPI; 1994-120230/15.
XX
XX Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region
XX
XX Example 1; Page 18; 230pp; English.
XX

```

Modification of a rodent antibody or fragment by resurfacing in order to produce a humanised rodent antibody can be determined by calculating homology between murine and human antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting, (2) resurfacing approach using most similar chain, and (3) resurfacing approach using human sequences with most similar surface residues. AAP52241-447 are the surface residue patterns in mouse heavy chain antibody variable regions. These "patches" were used in the third method, where rodent light and heavy chains were matched and the most similar human sequence found independently only over the surface residues indicated in AAP52030-67.

XX SQ Sequence 26 AA;

Query Match 100.0%; Score 26; DB 15; Length 26;
Best Local Similarity 100.0%; Pred No. 26-00; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
|||
Db 5 VLEP 8

RESULT 19

ABH31072
ID ABB31072 standard; Peptide; 27 AA.

XX AC ABB31072;

XX DT 01-FEB-2002 (first entry)

XX DE Peptide #3723 encoded by breast cell single exon nucleic acid probe.

XX FW Human; microarray; single exon probe; gene expression, breast, disease; cancer.

XX OS Homo sapiens.

XX PN WQ200157271-A2.

XX PD 09-AUG-2001;

XX PF 30-JAN-2001; 2001WO-0500662

XX PP 04-FEB-2000; 2000US-0180112

XX PR 26 MAY 2000; 2000US-0207456

XX PR 30-JUN-2000; 2000US-0609409

XX PR 03-AUG-2000; 2000US-0632366

XX PR 21-SEP-2000; 2000US-0234687

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000EP-0034263

XX FA (MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DP;

XX DR WPI; 2001-496933/54.

XX PT New spatially addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -

XX PS Claim 27, SEQ ID NO 14440, 327pp + sequence listing, English.

XX CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene

expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far fewer than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 20; DB 22; Length 27;

Best Local Similarity 100.0%; Pred No. 26-00; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
|||
Db 20 VLEP 23

RESULT 19

ABH36261
ID ABB36261 standard; Peptide; 27 AA.

XX AC ABB36261;

XX DT 04-FEB-2002 (first entry)

XX DE Peptide #3767 encoded by human foetal liver single exon probe.

XX FW Human; foetal liver; gene expression; single exon nucleic acid probe.

XX OS Homo sapiens.

XX PN WQ200157277-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-0500662.

XX PP 04-FEB-2000; 2000US-0180112.

XX PR 26 MAY 2000; 2000US-0207456.

XX PR 30-JUN-2000; 2000US-0609409.

XX PR 03-AUG-2000; 2000US-0632366.

XX PR 21-SEP-2000; 2000US-0234687.

XX PR 27-SEP-2000; 2000US-0236359.

XX PR 04-OCT-2000; 2000EP-0034263.

XX FA (MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DP;

XX DR WPI; 2001-483447/52.

XX PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human foetal liver -

XX PS Claim 27, SEQ ID NO 28806, 630pp + sequence listing, English.

XX CC The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human foetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.

XX Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX SQ Sequence 27 AA;

Query Match 100.0%; Score 20; DB 22; Length 27;
 Best Local Similarity 100.0%; Pred No. 2.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 20 VLEP 23

RESULT 20
 ABB21633
 ID ABB21633 standard; Protein; 27 AA.
 AC ABB21633;
 DT 23 JAN-2002 (first entry)
 XX
 XX Human brain expressed single exon probe for measuring heart cell gene expression;
 DE Protein #3612 encoded by probe for measuring heart cell gene expression;
 KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX
 XX Homo sapiens.
 CC W0200157275-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 20 JAN 2001; 2001W0 US00666.
 XX
 XX 04 FEB 2000; 2000US 0183312.
 XX
 XX 26 MAY 2000; 2000US 0207456.
 XX
 XX 30 JUN 2000; 2000US 0608408.
 XX
 XX 02 AUG 2000; 2000US 0633366.
 XX
 XX 21 SEP 2000; 2000US 0234687.
 XX
 XX 27 SEP 2000; 2000US 0236359.
 XX
 XX 04 OCT 2000; 2000EP 0024273.
 XX
 XX (MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DP;
 XX
 XX WPI, 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts -
 XX
 XX Claim 15, SEQ ID NO 23403; 530pp; English.
 XX
 XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ABA411305). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO
 CC at ftp.wipo.int/pub/published_pat_sequences.
 XX
 XX SQ Sequence 27 AA;
 XX
 XX Query Match 100.0%; Score 20; DB 22; Length 27;
 XX Best Local Similarity 100.0%; Pred No. 2.6e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 20 VLEP 23

RESULT 21
 AAM57035
 ID AAM57035 standard; Protein; 27 AA.
 XX
 XX AAM57035;
 XX
 XX 05-NOV-2001 (first entry)
 XX
 XX Human brain expressed single exon probe encoded protein SEQ ID NO: 29140.
 XX
 XX Human; brain expressed exon; gene expression analysis; probe;
 KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
 KW epilepsy; cancer.
 XX
 XX Homo sapiens.
 CC W0200157275-A2.
 XX
 XX 09-AUG-2001.
 XX
 XX 10 JAN 2001; 2001W0 US00667.
 XX
 XX 04 FEB 2000; 2000US 0183312.
 XX
 XX 26 MAY 2000; 2000US 0207456.
 XX
 XX 30 JUN 2000; 2000US 0608408.
 XX
 XX 02 AUG 2000; 2000US 0633366.
 XX
 XX 21 SEP 2000; 2000US 0234687.
 XX
 XX 27 SEP 2000; 2000US 0236359.
 XX
 XX 04 OCT 2000; 2000EP 0024273.
 XX
 XX (MOLECULAR DYNAMICS INC.
 XX
 XX Penn SG, Hanzel DK, Chen W, Rank DP;
 XX
 XX WPI, 2001-483446/52.
 XX
 XX Single exon nucleic acid probes for analyzing gene expression in human
 PT brains -
 XX
 XX Example 4; SEQ ID NO. 29140; 650pp; Sequence Listing, English.
 XX
 XX The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention.
 XX
 XX SQ Sequence 27 AA;
 XX
 XX Query Match 100.0%; Score 20; DB 22; Length 27;
 XX Best Local Similarity 100.0%; Pred No. 2.6e+02;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4
 ||||
 DB 20 VLEP 23

RESULT 22
 AAM69425
 ID AAM69425 standard; Protein; 27 AA.
 XX
 XX AAM69425;
 XX
 XX 06-NOV 2001 (first entry)
 XX
 XX Human bone marrow expressed probe encoded protein SEQ ID NO. 29731.
 XX
 XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.


```

XX PS Claim 27; SEQ ID NO 3025; 654pp, English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
CC see AA131315-AA157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.
XX
SQ Sequence 27 AA;
    Query Match 100.0%; Score 20; DB 22; Length 27;
    Best Local Similarity 100.0%; Pred No 2 25-32;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    QY 1 VLEP 4
    Db 20 VLEP 23

RESULT 25
AAM04951
ID AAM04951 standard; Protein; 27 AA.
XX
AC AAM04951;
XX
DT 09-OCT-2001 (first entry)
XX
DE Peptide #3633 encoded by probe for measuring breast gene expression.
XX
KW Probe, human, breast disease; breast cancer; development disorder;
XX inflammatory disease; proliferative breast disease; non-carcinoma tumour.
XX
OS Homo sapiens.
XX
PN NC0200157270.A2.
XX
PD 09-AUG-2001.
XX
PF 20-JAN-2001; 2001WG-US00661.
XX
PR 04-FEB-2000; 2000US 0180312.
XX 26 MAY 2000; 2000US 0207456.
XX 30-JUN-2000; 2000US-0608408
XX 03-AUG-2000; 2000US-0632366.
XX 21 SEP 2000; 2000US 0234587.
XX 27-SEP-2000; 2000US 0236359.
XX 04 OCT 2000; 2000JB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DP;
XX
XX WPI; 2001-476286/51.
XX
XX Novel single exon nucleic acid probe used to measuring gene expression
XX in a human breast -
XX
XX Claim 27, SEQ ID NO 13691; 322pp; English.
XX
CC The present invention relates to novel single exon nucleic acid probes
CC (see AA100010-AA110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic
CC aetiology. The diseases include: breast cancer; disorders of development,
CC inflammatory diseases of the breast; fibrocystic changes; proliferative
CC breast disease and non-carcinoma tumours.
CC Note. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO

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CC at ftp.wipo.int/pub/published_pat_sequences.

XX Sequence 27 AA;

Query Match 100.0%; Score 20; DB 22; Length 27;
Best Local Similarity 100.0%; Pred No 2 25-32;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

Db 20 VLEP 23

Search completed March 5, 2003, 08:22:09
Job time : 35 secs


```

; Sequence 15, Application US/09732411
; Patent No. US2002005839A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Adhesion Modulatory Peptides and Methods for Use
; FILE REFERENCE: EME 124CF
; CURRENT APPLICATION NUMBER: US/09/732,411
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 57/123,559
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: PPT/US00/10429
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-732-411-15

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 1 VLEP 4

RESULT 3
US-09-729-873-14
; Sequence 14, Application US/09729873
; Patent No. US2002003032A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Correspondin Derived Chemically- and Inhibitory Agents
; FILE REFERENCE: CMZ 131CF
; CURRENT APPLICATION NUMBER: US/09/729,873
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 57/123,754
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: PPT/US00/10344
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 6
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-729-873-14

Query Match 100.0%; Score 20; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 2 VLEP 5

RESULT 4
US-09-998-909-11
; Sequence 11, Application US/09998909
; Patent No. US2003016464A1
; GENERAL INFORMATION:
; APPLICANT: Hwang, John
; APPLICANT: Briggman, Joseph
; TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
; FILE REFERENCE: WTP-027
; CURRENT APPLICATION NUMBER: US/09/998,909
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/02/250,294
; PRIOR FILING DATE: 2000-11-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PPT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-998-909-11

Query Match 100.0%; Score 20; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 1 VLEP 4

RESULT 5
US-10-153-344-7
; Sequence 7, Application US/10153344
; Publication No. US20030004124A1
; GENERAL INFORMATION:
; APPLICANT: ROTHMAN, JOEL
; APPLICANT: BLOSS, TIM
; APPLICANT: WITZE, ERIC
; TITLE OF INVENTION: BTF3, AN INHIBITOR OF APOPTOSIS
; FILE REFERENCE: 407T-300410US
; CURRENT APPLICATION NUMBER: US/10/153,344
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US/02/002,559
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (10)-(10)
; OTHER INFORMATION: X is any amino acid
US-10-153-344-7

Query Match 100.0%; Score 20; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 VLEP 4
Db 6 VLEP 9

RESULT 6
US-09-956-206A-21
; Sequence 21, Application US/09056206A
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: DO COUTO, FERNANDO J.P.
; APPLICANT: GERANI, ROBERTO I.
; APPLICANT: PETERSON, JERRY A.
; TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
; M33 ANTI-B46 ANTIBODY, METHODS OF USE THEREOF, AND
; METHODS OF HUMANIZING ANTIBODY PEPTIDES
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & MORRISON
US-09-956-206A-21

```

STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1 0, Version #1 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/864,761
FILING DATE: 19-APR-2002
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/525,530
FILING DATE: 14-SEP-1995
APPLICATION NUMBER: PCT/US95/11693
FILING DATE: 14 SEP-1995
APPLICATION NUMBER: 08/487,508
FILING DATE: 7-JUNE-1995
APPLICATION NUMBER: 08/307,968
FILING DATE: 16-SEPT-1994
ATTORNEY/AGENT INFORMATION:
NAME: WITT, ERIC
REGISTRATION NUMBER: 44,408
REFERENCE/DOC# NUMBER: 276330000101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO. 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO. 21:
US 09-864-761-36931

Query Match 100.0%; Score 20; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 1 VLEP 4

RESULT 7
US-09-864-761-36931
Sequence 36931, Application US/09864761
Patent No. US20020049761A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DEPRIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aomic-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/00/180,332
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US/00/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US/00/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263-E
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US/00/236,359
PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-10
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36931
LENGTH: 27
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO A0007740.1
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.98
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.59
OTHER INFORMATION: EXPRESSED IN EPAIN, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.83
OTHER INFORMATION: EXPRESSED IN PT474, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.8
OTHER INFORMATION: EXPRESSED IN ACULT LIVER, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9e+02
US-09-864-761-36931

Query Match 100.0%; Score 20; DB 10; Length 27;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||
Db 20 VLEP 23

RESULT 8
US-09-920-552-45
Sequence 45, Application US/09920552
Patent No. US20020094576A1
GENERAL INFORMATION:
APPLICANT: Griffiths, David J.
APPLICANT: Weiss, Robin A.
APPLICANT: Venables, Patrick
TITLE OF INVENTION: Material
FILE REFERENCE: Abbott Labs
CURRENT APPLICATION NUMBER: US/09/320,553
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 09/299,329
PRIOR FILING DATE: 1999-03-29
PRIOR APPLICATION NUMBER: GB 0906649.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/115,288
PRIOR FILING DATE: 1999-01-08

NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 45
LENGTH: 28
TYPE: PRT
ORGANISM: Rous sarcoma virus
US-09 920 592-45

Query Match 100.0%, Score 20, DB 10, Length 29,
Best Local Similarity 100.0%, Pct 100.0,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 VLEP 4
DB 22 VLEP 25

RESULT 9
US-09-864-761-41269
Sequence 41269, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aecmeca X 1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2000-09-23
FILE APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/127,456
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/622,366
PRIOR FILING DATE: 2000-09-03
PRIOR APPLICATION NUMBER: GB 24263,1
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/235,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Ammax Sequence Listing Engine vers 1.1
SEQ ID NO 41269
LENGTH: 37
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: MAP TO AL133295.11
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN TESTIS, SIGNAL = 1.7
OTHER INFORMATION: PCT/HUMAN HIT: AM610487.1, EVALUATE 1 00e-15
US-09-864-761-41269

Query Match 100.0%, Score 20, DB 10, Length 37,
Best Local Similarity 100.0%, Pct 100.0,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 1 VLEP 4
DB 33 VLEP 36

RESULT 10
US-09-864-761-35818
Sequence 35818, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Aecmeca X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/237,456
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 09/630,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,1
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Ammax Sequence Listing Engine vers 1.1

1 SEQ ID NO 35818
2 LENGTH: 42
3 TYPE: PRT
4 ORGANISM: Homo sapiens
5 FEATURE:
6 OTHER INFORMATION: MAP TO AC009308.3
7 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL - 2
8 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL - 1.6
9 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL - 1.8
10 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 1.4
11 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 1.9
12 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 2
13 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 1.7
14 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL - 1.1
15 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2
16 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 1.6
17 OTHER INFORMATION: EST HUMAN HIT: A1108220.1, EVALUATION 3.60e+00
18 OTHER INFORMATION: SWISSPROT HIT: P17565, EVALUATION 3.60e+00

US-09-864-761-35818

Query March 100.0%, Score 20, PP 10, Length 42,
Best Local Similarity 100.0%, Pred. No. 1.5e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
DB 24 VLEP 27

RESULT 11
US-09-925-239-784

1 Sequence 784, Application US/09925239
2 Publication No. US20030040617A9
3 GENERAL INFORMATION:
4 APPLICANT: Posen et al.
5 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
6 FILE REFERENCE: PA102
7 CURRENT APPLICATION NUMBER: US/09/025,239
8 PRIOR FILING DATE: 2001-08-10
9 PRIOR APPLICATION NUMBER: PCT/US00/05983
10 PRIOR FILING DATE: 2000-03-08
11 PRIOR APPLICATION NUMBER: 60/124,270
12 PRIOR FILING DATE: 1999-03-12
13 NUMBER OF SEQ ID NOS: 1556
14 SOFTWARE: Patent In Ver. 2.0
15 SEQ ID NO 784
16 LENGTH: 44
17 TYPE: PRT
18 ORGANISM: Homo sapiens
19 US-09-925-239-784

Query March 100.0%, Score 20, PP 9, Length 44,
Best Local Similarity 100.0%, Pred. No. 1.5e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
DB 19 VLEP 22

RESULT 12
US-09-925-239-784

1 Sequence 784, Application US/09925239
2 Publication No. US20030040617A9
3 GENERAL INFORMATION:
4 APPLICANT: Posen et al.
5 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
6 FILE REFERENCE: PA102
7 CURRENT APPLICATION NUMBER: US/09/025,239
8 PRIOR FILING DATE: 2001-08-10
9 PRIOR APPLICATION NUMBER: PCT/US00/05983
10 PRIOR FILING DATE: 2000-03-08
11 PRIOR APPLICATION NUMBER: 60/124,270

1 PRIOR FILING DATE: 1999-03-12
2 NUMBER OF SEQ ID NOS: 1556
3 SOFTWARE: Patent In Ver. 2.0
4 SEQ ID NO 784
5 LENGTH: 44
6 TYPE: PRT
7 ORGANISM: Homo sapiens
8 US-09-925-239-784

Query March 100.0%, Score 20, PP 10, Length 44,
Best Local Similarity 100.0%, Pred. No. 1.5e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
DB 19 VLEP 22

RESULT 13

US-09-864-761-46702
1 Sequence 46702, Application US/09864761
2 Patent No. US20020040763A1
3 GENERAL INFORMATION:
4 APPLICANT: Penn, Sharron G.
5 APPLICANT: Rank, David R.
6 APPLICANT: Hanzel, David K.
7 APPLICANT: Chen, Wensheng

8 TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEOTIC ACID IN REG. US/09-864-761
9 FILE REFERENCE: Aemica-X-1
10 CURRENT APPLICATION NUMBER: US/09/864,761
11 PRIOR FILING DATE: 2001-09-23
12 PRIOR APPLICATION NUMBER: US 60/180,310
13 PRIOR FILING DATE: 2000-02-04
14 PRIOR APPLICATION NUMBER: US 60/207,456
15 PRIOR FILING DATE: 2000-05-26
16 PRIOR APPLICATION NUMBER: US 09/632,166
17 PRIOR FILING DATE: 2000-08-03
18 PRIOR APPLICATION NUMBER: GP 24263.6
19 PRIOR FILING DATE: 2000-10-04
20 PRIOR APPLICATION NUMBER: US 60/236,359
21 PRIOR FILING DATE: 2000-09-27
22 PRIOR APPLICATION NUMBER: PCT/US01/00666
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00667
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00664
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00669
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00665
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00668
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00663
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00662
37 PRIOR FILING DATE: 2001-01-30
38 PRIOR APPLICATION NUMBER: PCT/US01/00661
39 PRIOR FILING DATE: 2001-01-30
40 PRIOR APPLICATION NUMBER: PCT/US01/00670
41 PRIOR FILING DATE: 2001-01-30
42 PRIOR APPLICATION NUMBER: US 60/234,687
43 PRIOR FILING DATE: 2000-09-21
44 PRIOR APPLICATION NUMBER: US 09/604,408
45 PRIOR FILING DATE: 2000-06-30
46 PRIOR APPLICATION NUMBER: US 09/774,203
47 PRIOR FILING DATE: 2001-01-29
48 NUMBER OF SEQ ID NOS: 49117
49 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
50 SEQ ID NO 46702
51 LENGTH: 47
52 TYPE: PRT

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/ ORGANISM: Homo sapiens
/
/ FEATURE:
/
/ OTHER INFORMATION: MAP TO AF064863.1
/
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
/
/ OTHER INFORMATION: EXPRESSED IN HONE MARROW, SIGNAL = 1
/
/ OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
/
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.91
/
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
/
/ OTHER INFORMATION: SWISSPROT HIT: Q1043, EVALUPE # 606400
/
/ US 09 864 761 46702

Query Match 100.0%, Score 20, DP 10, Length 47,
Best Local Similarity 100.0%, Pval No. 1 6e-02,
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
|||||
DB 7 VLEP 10

RESULT 14
US-09-209-658-174
/ Sequence 174, Application US/09205658
/ Patent No. US2000032617A1
/ GENERAL INFORMATION:
/ APPLICANT: Ravkun, Gary
/ APPLICANT: G33, Scott
/ TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
/ TITLE OF INVENTION: IMPAIRED GLOUSH TISSUE CONDITIONS
/ FILE REFERENCE: 00786/351004
/ CURRENT APPLICATION NUMBER: US/09/209,659
/ CURRENT FILING DATE: 1998-12-03
/ EARLIER APPLICATION NUMBER: 08/857,076
/ EARLIER FILING DATE: 1997-05-15
/ EARLIER APPLICATION NUMBER: 08/888,534
/ EARLIER FILING DATE: 1997-07-07
/ EARLIER APPLICATION NUMBER: US98/10080
/ EARLIER FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 328
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NOS: 1-324
/ LENGTH: 49
/ TYPE: PRT
/ ORGANISM: Mus musculus or Homo sapiens or C elegans
/ US-09-205-658-174

Query Match 100.0%, Score 20, DP 10, Length 48,
Best Local Similarity 100.0%, Pval No. 1 6e-02,
Matches 4; Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 26 VLEP 29

RESULT 15
US 09 864 761 40223
/ Sequence 40223, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Bank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HGMAY GERMOME DERIVED SINGLE EXON NUCLEOTIDE AND PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aecmiga X 1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 1993-05-24
/ PRICE APPLICATION NUMBER: 60/180,312
/ PRICE FILING DATE: 2000-02-04
/ PRICE APPLICATION NUMBER: US 60/207,456
/ PRICE FILING DATE: 2000-05-26

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1 PRIOR APPLICATION NUMBER: US 69/180,312
2 PRIOR FILING DATE: 2000-02-04
3 PRIOR APPLICATION NUMBER: US 69/207,456
4 PRIOR FILING DATE: 2000-05-26
5 PRIOR APPLICATION NUMBER: US 69/632,366
6 PRIOR FILING DATE: 2000-08-01
7 PRIOR APPLICATION NUMBER: GR 24263.6
8 PRIOR FILING DATE: 2000-10-04
9 PRIOR APPLICATION NUMBER: US 69/236,359
10 PRIOR FILING DATE: 2000-09-27
11 PRIOR APPLICATION NUMBER: PCT/US01/00666
12 PRIOR FILING DATE: 2001-01-30
13 PRIOR APPLICATION NUMBER: PCT/US01/00667
14 PRIOR FILING DATE: 2001-01-30
15 PRIOR APPLICATION NUMBER: PCT/US01/00664
16 PRIOR FILING DATE: 2001-01-30
17 PRIOR APPLICATION NUMBER: PCT/US01/00669
18 PRIOR FILING DATE: 2001-01-30
19 PRIOR APPLICATION NUMBER: PCT/US01/00665
20 PRIOR FILING DATE: 2001-01-30
21 PRIOR APPLICATION NUMBER: PCT/US01/00662
22 PRIOR FILING DATE: 2001-01-30
23 PRIOR APPLICATION NUMBER: PCT/US01/00661
24 PRIOR FILING DATE: 2001-01-30
25 PRIOR APPLICATION NUMBER: PCT/US01/00670
26 PRIOR FILING DATE: 2001-01-30
27 PRIOR APPLICATION NUMBER: US 69/234,687
28 PRIOR FILING DATE: 2000-09-21
29 PRIOR APPLICATION NUMBER: US 69/608,408
30 PRIOR FILING DATE: 2000-06-30
31 PRIOR APPLICATION NUMBER: US 69/774,203
32 PRIOR FILING DATE: 2001-01-29
33 NUMBER OF SEQ ID NOS: 49117
34 SOFTWARE: Annonax Sequence Listing Engine vers 1.1
35 SEQ ID NO 37877
36 LENGTH: 52
37 TYPE: PRT
38 ORGANISM: Homo sapiens
39 FEATURE:
40 OTHER INFORMATION: MAP TO AC012140.1
41 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
42 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
43 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.96
44 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.1
45 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.99
46 OTHER INFORMATION: EXPRESSED IN HEPT, SIGNAL = 1.1
47 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
48 OTHER INFORMATION: SWISSPOT HIT: C75031, EVALUATION 0.006002
US-09-864-761-44895

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Query Match 100.0%; Score 20; DB 10; Length 52;
Best Local Similarity 100.0%; Pred No 1 del 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLEP 4
DB 9 VLEP 12

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RESULT 17

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US-09-864-761-44895
; Sequence 44895, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David P.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng

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; TITLE OF INVENTION: HUMAN GENE DERIVED SINGLE EXON NUCLEOTIC ACID SEQUENCE USEFUL FOR

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; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica X-1
; CURRENT APPLICATION NUMBER: US 69/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 69/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 69/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 69/632,366
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: GR 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 69/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 69/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 69/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 69/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonax Sequence Listing Engine vers 1.1
; SEQ ID NO 44895
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC019194.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EST HUMAN HIT: A4888971.1, EVALUATION 0.00625
; OTHER INFORMATION: SWISSPOT HIT: P77640, EVALUATION 0.00602
US-09-864-761-44895

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```

Query Match 100.0%; Score 20; DB 10; Length 53;
Best Local Similarity 100.0%; Pred No 1 del 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 VLEP 4
DB 31 VLEP 34

```

RESULT 18

```

US-09-925-300-1385
; Sequence 1385, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Craig Rosen.
; APPLICANT: Steve Eden

```

```

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/025,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 69/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1385
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: 1591
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300 1385

Query Match: 100.0%, Score 20, DB 10, Length 56;
Best Local Similarity 100.0%, Freq. No. 1.9e+02,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0,

QY 1 VLEP 4
DB 30 VLEP 33

RESULT 19
US-09-864-761-34003
; Sequence 34003, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DEVELOPED SINGLE ENYM NUCLEIC ACID PROBE USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 69/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24003,5
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

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; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34003
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ACC06017.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN PCNE MAPPW, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.91
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BEAS, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEPT, SIGNAL = 0.93
; OTHER INFORMATION: EST HUMAN HIT: AW370405.1, EVALUATE 0.00e-20
; OTHER INFORMATION: SWISSPROT HIT: Q011F2, EVALUATE 4.40e+00
US-09-864-761-34003

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Query Match: 100.0%, Score 20, DB 10, Length 61;
Best Local Similarity 100.0%, Freq. No. 2.1e+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

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QY 1 VLEP 4

DB 29 VLEP 32

RESULT 20

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US-09-864-761-43009
; Sequence 43009, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DEVELOPED SINGLE ENYM NUCLEIC ACID PROBE USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 69/832,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24003,5
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30

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1 PRIOR APPLICATION NUMBER: PCT/US01/00663
2 PRIOR FILING DATE: 2001-01-30
3 PRIOR APPLICATION NUMBER: PCT/US01/00662
4 PRIOR FILING DATE: 2001-01-30
5 PRIOR APPLICATION NUMBER: PCT/US01/00661
6 PRIOR FILING DATE: 2001-01-30
7 PRIOR APPLICATION NUMBER: PCT/US01/00670
8 PRIOR FILING DATE: 2001-01-30
9 PRIOR APPLICATION NUMBER: US 60/234,687
10 PRIOR FILING DATE: 2000-09-21
11 PRIOR APPLICATION NUMBER: US 09/608,408
12 PRIOR FILING DATE: 2000-04-13
13 PRIOR APPLICATION NUMBER: US 09/774,203
14 PRIOR FILING DATE: 2001-01-29
15 NUMBER OF SEQ ID NOS: 49117
16 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
17 SEQ ID NO 43309
18 LENGTH: 63
19 TYPE: PRT
20 ORGANISM: Homo sapiens
21 FEATURE:
22 OTHER INFORMATION: MAP TO AC004108.1
23 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.71
24 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.61
25 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.75
26 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
27 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.65
28 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.78
29 OTHER INFORMATION: SWISSPROT HIT: P32595, EVALUE 6.80e-01
30 OTHER INFORMATION: PCT_HUMAN HIT: P67516, EVALUE 9.70e-01
31 US-09-864 761-43309

Query Match 100.0% Score 20; DR 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 23 VLEP 26

RESULT 21
US-09-864-761-43309
1 Sequence 17, Application US/09864761
2 Patent No. US20020048962A1
3 GENERAL INFORMATION:
4 APPLICANT: Inouye, Sumiko
5 APPLICANT: Inou, Wei-Yin
6 APPLICANT: Eagle, Susan
7 APPLICANT: Inouye, Masayori
8 TITLE OF INVENTION: POLYMER-TIC REVERSE TRANSCRIPTASE
9 NUMBER OF SEQUENCES: 52
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: WEISER & ASSOCIATES
12 STREET: 230 South Fifteenth Street, Suite 500
13 CITY: Philadelphia
14 STATE: PA
15 COUNTRY: USA
16 ZIP: 19102
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: WINDOWS DOS
21 SOFTWARE: Patent in Release #1.0, Version #1.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/09/098,031A
24 FILING DATE: 03-MAR-1997
25 CLASSIFICATION: 435
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Weiser, Gerard J.
28 REGISTRATION NUMBER: 19,763
29 REFERENCE/DOCKET NUMBER: 377(913).5888P
30 TELECOMMUNICATION INFORMATION:

1 TELEPHONE: 215-875-8383
2 TELEFAX: 215-875-8394
3 INFORMATION FOR SEQ ID NO: 17:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 65 amino acids
6 TYPE: amino acid
7 STRAIDEDNESS:
8 TOPOLOGY: linear
9 MOLECULE TYPE: protein
10 US-08-808-031A-17

Query Match 100.0% Score 20; DR 8; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

DB 24 VLEP 27

RESULT 22
US-09-864-761-39828
1 Sequence 39828, Application US/09864761
2 Patent No. US20020048763A1
3 GENERAL INFORMATION:
4 APPLICANT: Penn, Sharron G.
5 APPLICANT: Penn, David P.
6 APPLICANT: Hanzel, David K.
7 APPLICANT: Chen, Wensheng
8 TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
9 FILE REFERENCE: Aemica-X-1
10 CURRENT APPLICATION NUMBER: US/09/864,761
11 PRIOR FILING DATE: 2001-05-23
12 PRIOR APPLICATION NUMBER: US 60/180,312
13 PRIOR FILING DATE: 2000-02-04
14 PRIOR APPLICATION NUMBER: US 60/207,456
15 PRIOR FILING DATE: 2000-05-26
16 PRIOR APPLICATION NUMBER: US 09/632,166
17 PRIOR FILING DATE: 2000-08-03
18 PRIOR APPLICATION NUMBER: GB 24263.6
19 PRIOR FILING DATE: 2000-10-04
20 PRIOR APPLICATION NUMBER: US 60/236,159
21 PRIOR FILING DATE: 2000-09-27
22 PRIOR APPLICATION NUMBER: PCT/US01/00666
23 PRIOR FILING DATE: 2001-01-30
24 PRIOR APPLICATION NUMBER: PCT/US01/00667
25 PRIOR FILING DATE: 2001-01-30
26 PRIOR APPLICATION NUMBER: PCT/US01/00664
27 PRIOR FILING DATE: 2001-01-30
28 PRIOR APPLICATION NUMBER: PCT/US01/00669
29 PRIOR FILING DATE: 2001-01-30
30 PRIOR APPLICATION NUMBER: PCT/US01/00665
31 PRIOR FILING DATE: 2001-01-30
32 PRIOR APPLICATION NUMBER: PCT/US01/00668
33 PRIOR FILING DATE: 2001-01-30
34 PRIOR APPLICATION NUMBER: PCT/US01/00663
35 PRIOR FILING DATE: 2001-01-30
36 PRIOR APPLICATION NUMBER: PCT/US01/00662
37 PRIOR APPLICATION NUMBER: PCT/US01/00661
38 PRIOR FILING DATE: 2001-01-30
39 PRIOR APPLICATION NUMBER: PCT/US01/00670
40 PRIOR FILING DATE: 2001-01-30
41 PRIOR APPLICATION NUMBER: US 60/234,687
42 PRIOR FILING DATE: 2000-09-21
43 PRIOR APPLICATION NUMBER: US 09/608,408
44 PRIOR FILING DATE: 2000-06-30
45 PRIOR APPLICATION NUMBER: US 09/774,203
46 PRIOR FILING DATE: 2001-01-29
47 NUMBER OF SEQ ID NOS: 49117
48 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
49 SEQ ID NO 39828

LENGTH: 65
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005939.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.8
OTHER INFORMATION: EST HUMAN HIT: BP28034, EVALUATE 1.00e 01
OTHER INFORMATION: SWISSPOT HIT: Q14514, EVALUATE 3.00e 00
US-09-864-761-39829
Query Match: 100.0%, Score 20, DB 10, Length 65,
Best Local Similarity: 100.0%, Ref: No. 2, 3e+02,
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 1 VLEP 4
DB 36 VLEP 39
RESULT 23
US-09-864-761-42067
Sequence 42067, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David P.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID SEQUENCE REFIL FOR
FILE REFERENCE: Aestica X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 42067
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL049780.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.7
OTHER INFORMATION: EST HUMAN HIT: AW50015, EVALUATE 5.00e-35
OTHER INFORMATION: SWISSPOT HIT: P21800, EVALUATE 1.00e-04
US-09-864-761-42067
Query Match: 100.0%, Score 20, DB 10, Length 66;
Best Local Similarity: 100.0%, Ref: No. 3, 3e+02;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 1 VLEP 4
DB 25 VLEP 28
RESULT 24
US-09-864-761-48913
Sequence 48913, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David P.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID SEQUENCE REFIL FOR
FILE REFERENCE: Aestica X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30

1 PRIOR APPLICATION NUMBER: PCT/US01/06670
2 PRIOR FILING DATE: 2001-01-10
3 PRIOR APPLICATION NUMBER: US 60/234,687
4 PRIOR FILING DATE: 2000-09-21
5 PRIOR APPLICATION NUMBER: US 09/608,408
6 PRIOR FILING DATE: 2000-06-10
7 PRIOR APPLICATION NUMBER: US 09/774,203
8 PRIOR FILING DATE: 2001-01-20
9 NUMBER OF SEQ ID NOS: 49117
10 SOFTWARE: Anomax Sequence Listing Engine vers 1.1
11 SEQ ID NO 48911
12 LENGTH: 67
13 TYPE: PRT
14 ORGANISM: Homo sapiens
15 FEATURE:
16 OTHER INFORMATION: MAP TO AL121716.2
17 OTHER INFORMATION: EXPRESSED IN R1474, SIGNAL = 1
18 OTHER INFORMATION: SWISSEPT HIT: Cx33pc, EVALUATE 1.000 00
19 OTHER INFORMATION: EST_HUMAN HIT: AA625526.1, EVALUATE 3.000 10
20 US-09-864-761-48913

Query Match 100.0%; Score 20; DP 10; Length 67;
Best Local Similarity 100.0%; Pred No 2 3e+22;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
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Db 15 VLEP 18

RESULT 25

US-09-925-301-1660
1 Sequence 1660, Application US/09925301
2 Patent No. US20020052308A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
6 FILE REFERENCE: PA106
7 CURRENT APPLICATION NUMBER: US/09/925,301
8 CURRENT FILING DATE: 2001-08-10
9 PRIOR APPLICATION NUMBER: PCT/US00/05882
10 PRIOR FILING DATE: 2000-03-08
11 PRIOR APPLICATION NUMBER: 60/124,270
12 PRIOR FILING DATE: 1999-03-12
13 NUMBER OF SEQ ID NOS: 1694
14 SOFTWARE: Patent In Ver. 2.0
15 SEQ ID NO 1660
16 LENGTH: 68
17 TYPE: PRT
18 ORGANISM: Homo sapiens
19 FEATURE:
20 NAME/KEY: SITE
21 LOCATION: (9)
22 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
23 NAME/KEY: SITE
24 LOCATION: (12)
25 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
26 NAME/KEY: SITE
27 LOCATION: (20)
28 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
29 NAME/KEY: SITE
30 LOCATION: (21)
31 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
32 NAME/KEY: SITE
33 LOCATION: (24)
34 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
35 NAME/KEY: SITE
36 LOCATION: (25)
37 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
38 NAME/KEY: SITE
39 LOCATION: (29)
40 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
41 NAME/KEY: SITE

1 LOCATION: (39)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
3 NAME/KEY: SITE
4 LOCATION: (45)
5 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
6 NAME/KEY: SITE
7 LOCATION: (51)
8 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
9 NAME/KEY: SITE
10 LOCATION: (52)
11 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
12 NAME/KEY: SITE
13 LOCATION: (66)
14 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
15 US-09-925-301-1660

Query Match 100.0%; Score 20; DP 10; Length 68;
Best Local Similarity 100.0%; Pred No 3 3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
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Db 56 VLEP 59

Search completed: March 5, 2003, 08:37:51
Job time : 14 secs



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OM protein - protein search, using sw mod-1

Run on: Match 5, 2003, on 11:35, Search time 14 seconds
(without alignments)
8,407 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BLASTW62

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Searched: 262574 seqs, 20420222 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database:

Issued Patents AA:*

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2: /cgn2_6/prodata/1/1aa/6B/OWB pep.*

3: /cgn2_6/prodata/1/1aa/6A/OWB pep.*

4: /cgn2_6/prodata/1/1aa/6B/OWB pep.*

5: /cgn2_6/prodata/1/1aa/6C/OWB pep.*

6: /cgn2_6/prodata/1/1aa/6D/OWB pep.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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2	20	100.0	19	4	US-08-928-213R-15
3	20	100.0	19	4	US-08-001-944C-72
4	20	100.0	25	1	US-08-137-404-20
5	20	100.0	25	2	US-08-453-353-20
6	20	100.0	25	3	US-08-011-591-5
7	20	100.0	26	1	US-07-942-245-281
8	20	100.0	26	4	US-08-536-630A-21
9	20	100.0	34	2	US-08-067-508-1
10	20	100.0	34	3	US-08-067-508-1
11	20	100.0	34	5	US-08-02552-1
12	20	100.0	35	4	US-08-082-070P-504
13	20	100.0	35	4	US-08-315-104R-504
14	20	100.0	40	4	US-08-314-268-106
15	20	100.0	65	6	US-08-058-17
16	20	100.0	70	4	US-08-134-001C-4570
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18	20	100.0	87	4	US-08-655-270A-25
19	20	100.0	93	3	US-08-208-804-3
20	20	100.0	93	3	US-08-801-743-3
21	20	100.0	98	3	US-08-478-097A-5
22	20	100.0	100	2	US-08-063-601-2
23	20	100.0	105	3	US-08-488-551R-610
24	20	100.0	108	3	US-08-388-353-639
25	20	100.0	112	3	US-08-027-413-7
26	20	100.0	114	1	US-08-481-377-27
27	20	100.0	114	2	US-08-491-846-25

28	20	100.0	114	3	US-09-153-733A-27
29	20	100.0	114	3	US-08-040-002A-26
30	20	100.0	114	4	US-08-172-062-26
31	20	100.0	114	4	US-09-302-520D-25
32	20	100.0	114	4	US-08-380-705-27
33	20	100.0	114	5	PCT-US94-02552-27
34	20	100.0	114	5	PCT-US94-00685-25
35	20	100.0	120	4	US-08-485-953-2
36	20	100.0	126	4	US-08-134-001C-4570
37	20	100.0	128	4	US-08-935-223-306
38	20	100.0	128	4	US-08-431-248A-8
39	20	100.0	130	1	US-08-426-627-18
40	20	100.0	130	4	US-08-367-953B-114
41	20	100.0	133	4	US-08-367-953B-118
42	20	100.0	139	4	US-08-367-953B-131
43	20	100.0	143	3	US-08-725-459B-43
44	20	100.0	156	3	US-08-826-246-10
45	20	100.0	156	3	US-08-944-495-10
46	20	100.0	156	3	US-08-126-540-11
47	20	100.0	156	4	US-08-925-588-10
48	20	100.0	156	4	US-08-288-292A-31
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50	20	100.0	161	3	US-08-126-540-11

ALIGNMENTS

RESULT 1

US-08-737-109-5

Sequence 5, Application US/08/37109

Patent No. 6455688

GENERAL INFORMATION:

APPLICANT: SLARAS, Antoni Ryszard

APPLICANT: ELBOPOLSK, Kieran Michael

APPLICANT: BRIGHT, Simon William Jonathan

APPLICANT: FENTEM, Philip Anthony

TITLE OF INVENTION: Plant Gene Specifying Acetyl Coenzyme A

TITLE OF INVENTION: Carboxylase and Transformed Plants Containing Same

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.

STREET: 1100 New York Avenue, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette

COMPUTER: IBM PC compatible

OPERATING SYSTEM: P-PC2/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/737,109

FILING DATE: 21-OCT-1996

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB94/50846

FILING DATE: 02-MAY-1994

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Avena sativa

US-08-737-109-5

Query Match 100.0%, Score 20, DB 4, Length 9;

Best Local Similarity 100.0%, Pred No. 19e-05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VLEP	4
Db	2	VLEP	5

RESULT 2

US-08-928-213B-35
Sequence 35, Application US-08-928213B
Patent No. 623905
GENERAL INFORMATION
APPLICANT: McHenry, Charles S.
Seville, Mark
Cull, Millard G.
TITLE OF INVENTION: NOVEL THERMOFILIC POLYMERASE III
HOLOENZYME
NUMBER OF SEQUENCES: 195
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCELLEN & CARROLL, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104

US-08-929 0035 35

Query Match:	100.0%	Score 20	DB 4	Length 19
Best Local Similarity	100.0%	Pred. NS: 72		
Matches	4	Conservative	0	Mismatches 0

Qy	1	VLEP	4
Db	1	VLEP	4

RESULT 3

```

US-39-001-984C-72
RESULT 3
Sequence 72, Application US/09001984C
Patent No. 6245331
GENERAL INFORMATION
APPLICANT: Lael, Suman
APPLICANT: Zella-Pazner, Susan
APPLICANT: Belislie, John T
TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
FILE REFERENCE: NYU-011
CURRENT APPLICATION NUMBER: US/09/001,984C
CURRENT FILING DATE: 1997-12-31
PRIOR APPLICATION NUMBER: 62/014,003
PRIOR FILING DATE: 1996-12-01

```

```

; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-001-984C-72

```

Query Match 100.0%; Score 20; DP 4; Length 19;
Best local Similarity 100.0%, Prod No. 72,
Matches 4; Conservative 0; Mismatches 0; Indels

QY	1	VLEP	4
Dh	15	VLEP	18

RESULT 4

```

1  US 08/127,909-20
2  Sequence No. Application US/08/127909
3  Patent No. 5436228
4  GENERAL INFORMATION:
5  APPLICANT: Postlethwaite, Arnold E.
6  APPLICANT: Seyer, Jerome
7  APPLICANT: Kang, Andrew
8  TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
9  NUMBER OF SEQUENCES: 20
10 CORRESPONDENCE ADDRESS:
11 ADDRESSES: Scully, Scott, Murphy & Presser
12 STREET: 400 Garden City Plaza
13 CITY: Garden City
14 STATE: New York
15 COUNTRY: U.S.A.
16 ZIP: 11530
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC Compatible
20 HEALING SYSTEM FOR TCS/MS-FOS
21 SOFTWARE: Patent In Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/127,909
24 FILING DATE:

```

```
?  
? FIELDS DATA:  
? CLASSIFICATION: 530  
? ATTORNEY/AGENT INFORMATION:  
? NAME: DiGiglio, Frank S.  
? REGISTRATION NUMBER: 31,346  
? REFERENCE/DOCKET NUMBER: 98002  
? TELECOMMUNICATION INFORMATION:  
? TELEPHONE: (516) 742-4343  
? TELEFAX: (516) 742-4366  
? TELEX: 238 901 SANS UR  
? INFORMATION FOR SET ID NO.: 00  
? SEQUENCE CHARACTERISTICS:  
? LENGTH: 25 amino acids  
? TYPE: amino acid  
? TOPOLOGY: linear  
? MOLECULE TYPE: peptide  
? UN-08-127-909-20
```

Query Match 100.0%; Score 20; DB 1; Length 25;
Best Local Similarity 100.0%; Pred No 95;
Matches 4; Conservative 0; Mismatches 0; Indels

Qy	1	VLEP	4
Db	4	VLEP	7

RESULT 5

US-08-457-353-20
; Sequence no, Application US/08457353
; Patent No. 5824647
; GENERAL INFORMATION:

APPLICANT: Postlethwaite, Arnold E.
APPLICANT: Sevier, Jerome
APPLICANT: Kang, Andrew
TITLE OF INVENTION: CHEMOTACTIC WOUND HEALING PEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.05
CURRENT APPLICATION NUMBER: US/98/457,353
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,146
REFERENCE/DOCYET NUMBER: 9202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 09 457-353-20

Query Match 100.0%; Score 20; DB 2; Length 25;
Best Local Similarity 100.0%; Pred No 05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 4 VLEP 7

RESULT 6
US-09-011-525-5
Sequence 5, Application US/99011525
GENERAL INFORMATION:
APPLICANT: BOTH, GERALD W.
TITLE OF INVENTION: GENE THERAPY USING OVINE ADENOVIRAL VECTORS
FILE REFERENCE: Gene Therapy Using Ovine Adenoviral Ve
CURRENT APPLICATION NUMBER: JC/69/011,525
CURRENT FILING DATE: 1998-04-20
EARLIER APPLICATION NUMBER: PCT/AUSK/00519
EARLIER FILING DATE: 1996-08-14
EARLIER APPLICATION NUMBER: AU PN4776
EARLIER FILING DATE: 1995-09-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 25
TYPE: PRT
ORGANISM: Ovine adenovirus
US-09-011-525-5

Query Match 100.0%; Score 20; DB 3; Length 25;
Best Local Similarity 100.0%; Pred No 05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4

Db 7 VLEP 10
RESULT 7
US 07-942-245-281
Sequence 281, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:
APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen M.J.
APPLICANT: REES, Anthony R.
APPLICANT: ROGUSKA, Michael A.
APPLICANT: GUILD, Braydon C.
TITLE OF INVENTION: SURFACE PEPTIDE VECTORS
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughue, Michl, Zirm, Maspeck & Seag
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: United States
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09 SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 281:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 07 942-245-281

Query Match 100.0%; Score 20; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 92,
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 5 VLEP 8

RESULT 8
US-08-525-539A-21
Sequence 21, Application US/0805539A
Patent No. 6309636
GENERAL INFORMATION:
APPLICANT: BOGOTTO, FERNANDO J.R.
APPLICANT: CERIANI, ROBERTO L.
APPLICANT: PETERSON, JERRY A.
TITLE OF INVENTION: RECOMBINANT PEPTIDES DERIVED FROM THE
TITLE OF INVENTION: M3 ANTI-BAG6 ANTIBODY, METHODS OF USE THEREOF, AND
TITLE OF INVENTION: METHODS OF HUMANIZING ANTIBODY PEPTIDES
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & MORRISON
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/96/525,539A
FILING DATE: 14-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DYLAN, TYLER
REGISTRATION NUMBER: 37,612
REFERENCE/POCKET NUMBER: 274,333-2210
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO. 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-525-539A 21

Query Match 100.0%, Score 20, DB 4, Length 26,
Best Local Similarity 100.0%, Pred. No. 99,
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 1 VLEP 4

RESULT 9
US-08-967-508-1
Sequence 1, Application US/08967508
Patent No. 5910570
GENERAL INFORMATION:
APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elihammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP GalNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,508
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 5910570ember 1995
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/POCKET NUMBER: 4755.P CP
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-508-1

Query Match 100.0%, Score 20, DB 4, Length 26,
Best Local Similarity 100.0%, Pred. No. 99+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 1 VLEP 4

SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-508-1

Query Match 100.0%, Score 20, DB 2, Length 34;
Best Local Similarity 100.0%, Pred. No. 130+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 7 VLEP 10

RESULT 10
US-08-967-506-1
Sequence 1, Application US/08967506
Patent No. 6096512
GENERAL INFORMATION:

APPLICANT: The Upjohn Company
APPLICANT: FOR U.S. PURPOSES ONLY: Elihammer, Ake P. and Homa, Fred L.
TITLE OF INVENTION: A Cloned DNA Encoding a UDP GalNAc:
TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company, Intellectual
ADDRESSEE: Property Legal Services
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,506
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,830
FILING DATE: 13 No. 6096512ember 1995
ATTORNEY/AGENT INFORMATION:
NAME: Darnley Jr., James D.
REGISTRATION NUMBER: 33,673
REFERENCE/POCKET NUMBER: 4755.P CP
TELEPHONE: 616-833-2210
TELEFAX: 616-833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-506-1

Query Match 100.0%, Score 20, DB 3, Length 34;
Best Local Similarity 100.0%, Pred. No. 130+02;
Matches 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||||
DB 7 VLEP 10


```
RESULT 11.
PCT-US94-02552-1
; Sequence 1, Application PC/TUS9402552
; GENERAL INFORMATION:
; APPLICANT: Elhammer, Ale P
; APPLICANT: Homa, Fred L
; TITLE OF INVENTION: A cloned cDNA encoding a NAD GalNA-
; TITLE OF INVENTION: Polypeptide, N-Acetylgalactosaminyltransferase
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Upjohn Company, Corp. Intellectual
; ADDRESSEE: Property Law
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: Michigan
; COUNTRY: USA
; ZIP: 49001
; COMPUTER READABLE FORM.
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1 0, Version #1 25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02552
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Darnley Jr., James D.
; REGISTRATION NUMBER: 33,673
; REFERENCE/BOOK NUMBER: 4755 P 7P
; TELECOMMUNICATION INFORMATION
; TELEPHONE: 616-385-5210
; TELEFAX: 616-385-6897
; TELEX: 224401
; INFORMATION FOR SEQ ID NO. 1:
; SEQUENCE CHARACTERISTICS
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US94-02552-1
;
Query Match 100.0%; Score 20; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLEP 4
Db 7 VLEP 10

RESULT 12
US-09-092-279B-504
; Sequence 504, Application US/09092279B
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH PHRANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/092,279B
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence

PCT-US94-02552-1
;
Query Match 100.0%; Score 20; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLEP 4
Db 7 VLEP 10
```

```
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-504
;
Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLEP 4
Db 13 VLEP 16

RESULT 13
US-09-315-304B-504
; Sequence 504, Application US/0915304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMA KINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 05/092,279
; PTO/FILING DATE: 1994-06-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 504
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-504
;
Query Match 100.0%; Score 20; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 VLEP 4
Db 13 VLEP 16

RESULT 14
US-09-314-268-106
; Sequence 106, Application US/09014268
; Patent No. 6346377
; GENERAL INFORMATION:
; APPLICANT: Doorbar, John
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO SCREENING FOR FATIGUE
; TITLE OF INVENTION: VIRUSES
; FILE REFERENCE: 3789/80902
; CURRENT APPLICATION NUMBER: US/09/314,268
; CURRENT FILING DATE: 1999-03-10
; EARLIER APPLICATION NUMBER: 09/314,269
; EARLIER FILING DATE: 1999-05-18
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 106
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Human papillomavirus type 30
US-09-314-268-106
;
Query Match 100.0%; Score 20; DB 4; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	VLEP	4
DL	19	VLEP	22

RESULT 15
5320958 17
PATENT NO. 5320958
APPLICANT: INUYAMA, JUNICHI, HBU, MEI YIN, EASLE, SUSAN,
INUYAMA, MASAYUKI
TITLE OF INVENTION: ISOLATED BACTERIAL REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/315,310
FILING DATE: 24 FEB.1989
SEQ ID NO.17
LENGTH: 65
5320958-17

```

RESULT 16
US-09-134-001C-4579
Sequence 4579, Application US/09134001C
Patent NO. 6383370
GENERAL INFORMATION
APPLICANT: LYNN DOUCETTE-STAMM et al
TITLE OF INVENTION: NOVEL ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US-09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRICE APPLICATION NUMBER: US 60/555,773
PRICE FILING DATE: 1997-08-14
NUMBER OF SEQ. IN NOS: 5674
SEQ ID NO 4579
LENGTH: 70
TYPE: PKT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4579

```

```

1 RESULT 17
2 US-08-928-383B-13
3 US-08-928-383B-13
4 : Sequence 13, Application US/88928383B
5 : Patent No. 6210211
6 :
7 : GENERAL INFORMATION:
8 : APPLICANT: Robert W. Finberg, Jeffrey M. Bergelson,
9 : APPLICANT: and Marshall S. Horwitz
10 : TITLE OF INVENTION: CAP, A NO. 6210211 COMBINATION OF COCAINE AND ALCOHOL
11 : TITLE OF INVENTION: CAP, A NO. 6210211 COMBINATION OF COCAINE AND ALCOHOL
12 : NUMBER OF SEQUENCES: 26
13 : CORRESPONDENCE ADDRESS:
14 : ADDRESSES: LAHIVE & COCKFIELD, LLP
15 : STREET: 28 State Street

```

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,383B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PPIC APPLICATION DATA:
APPLICATION NUMBER: US 60/026,100
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DPN-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)237-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 75 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-928-383B-13

```

1 RESULT 18
2 US-09-655-270A-25
3     Sequence 25, Application US-09655270A
4     Patent No. 6329151
5     GENERAL INFORMATION:
6     APPLICANT: Rouviere, Pierre E.
7     TITLE OF INVENTION: High Density Sampling
8     CURRENT APPLICATION NUMBER: US-09/655,270A
9     CURRENT FILING DATE: 2000-09-05
10    PRIOR APPLICATION NUMBER: 69/120,762
11    PRIOR FILING DATE: 1998-February-19
12    PRICE APPLICATION NUMBER: 60/152,542
13    PRICE FILING DATE: 1998-September-03
14    NUMBER OF SEQ ID NOS: 37
15    SOFTWARE: Microsoft Office 97
16    SEQ ID NO 25
17    LENGTH: 82
18    TYPE: PRT
19    ORGANISM: Unknown Organism
20    FEATURE:
21    OTHER INFORMATION: Description of Unknown
22    OTHER INFORMATION: not one single organism
23    US-09-655-270A-25

```

```

RESULT 19
US-09-208-804-3
; Sequence 3, Application US/09208804
; Patent No. 6030826
; GENERAL INFORMATION:
; APPLICANT: Au Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN PAPULIN LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/208,804
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/801,743
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF 0217 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 693800
; US-09-208-804-3

```

```

Query Match 100.0%; Score 20; DB 3; Length 93;
Best Local Similarity 100.0%; Freq No 3 Re:02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4
DB 71 VLEP 74

RESULT 20
US-08-801-743-3
; Sequence 3, Application US/08801743
; Patent No. 6037164
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; TITLE OF INVENTION: NOVEL HUMAN PAPULIN LIKE PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,743
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0217 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 693800
; US-08-801-743-3

Query Match 100.0%; Score 20; DB 3; Length 93;
Best Local Similarity 100.0%; Freq No 3 Re:02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 1 VLEP 4
DB 71 VLEP 74

RESULT 21
US-08-478-097A-5
; Sequence 5, Application US/08478097A
; Patent No. 6040431
; GENERAL INFORMATION:
; APPLICANT: KECK, PETER
; APPLICANT: SMART, JOHN
; TITLE OF INVENTION: SINGLE-CHAIN ANALOGS OF TGF-B
; TITLE OF INVENTION: SUPERFAMILY (MORPHONS)
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATION, TESTA, HEFWEITZ &
; ADDRESS: THIBEAULT, LLP
; STREET: 125 HIGH STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.05
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,097A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER ESQ, EDMUND R
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: GPP-080
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7000
; TELEFAX: 617-248-7100

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; INFORMATION FOR SEQ ID NO. 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1-98
; OTHER INFORMATION: /note="TGF-R5 SEQUENCE"
US-08-478-097A-5

Query Match 100.0% Score 20; DB 3; Length 98;
Best Local Similarity 100.0%; Pred No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 68 VLEP 71

RESULT 22
US-08-963-601-2
; Sequence 2, Application US/08963601
; Patent No. 5939528
; GENERAL INFORMATION:
; APPLICANT: CLAPPY, JIM C
; APPLICANT: CHOI, JUNGWON
; TITLE OF INVENTION: CRYSTALLINE FGF COMPLEX
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: APIAD Pharmaceuticals, Inc.
; STREET: 26 Lansdowne Street
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02139-4234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1 0, Version #1 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/963,601
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/735,848
; FILING DATE:
; APPLICATION NUMBER: US 60/005,808
; FILING DATE: 23-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/006,069
; FILING DATE: 24-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: BERNSTEIN, David L
; REGISTRATION NUMBER: 31,235
; REFERENCE/DOCYET NUMBER: APIAD 350A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-494-0400
; TELEFAX: 617-494-0208
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-963-601-2

Query Match 100.0% Score 20; DB 2; Length 100;
Best Local Similarity 100.0%; Pred No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 84 VLEP 87

RESULT 24
US-08-388-353-639
; Sequence 639, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.

Query Match 100.0% Score 20; DB 3; Length 105;
Best Local Similarity 100.0%; Pred No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 84 VLEP 87

RESULT 23
US-08-488-551B-639
; Sequence 639, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-8299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4092 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM321/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCYET NUMBER: 96062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 639:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-488-551B-639

Query Match 100.0% Score 20; DB 3; Length 105;
Best Local Similarity 100.0%; Pred No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
DB 84 VLEP 87

RESULT 24
US-08-388-353-639
; Sequence 639, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.

```

APPLICANT: Learmont, Jennifer C.
 APPLICANT: McPhee, Dale A.
 APPLICANT: Crowe, Suzanne
 APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV 1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Scully, Scott, Murphy & Fresser
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: us/oa/aa,353
 FILING DATE: 14-FEB-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Digiglio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 9606
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 TELEFAX: (516) 742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 639:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 108 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-388-353-639

Query Match 100.0%; Score 20; DB 3; Length 108;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 84 VLEP 87

RESULT 25

US-08-927-433-7
 Sequence 7, Application US/08927433
 Patent No. 6107476

GENERAL INFORMATION:

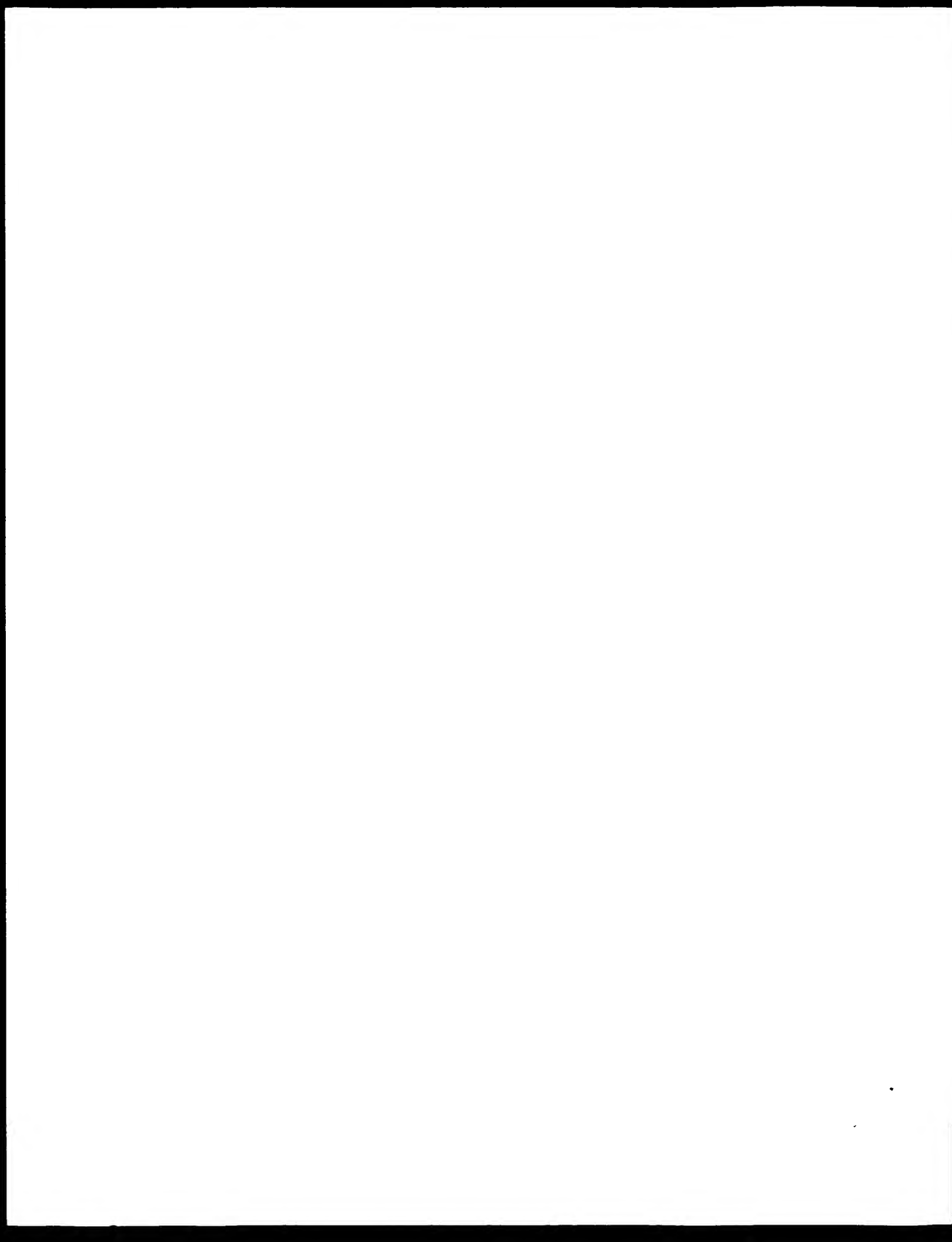
APPLICANT: Erlander, Mark G.
 APPLICANT: Huang, Shaoming
 APPLICANT: Jackson, Michael A.
 APPLICANT: Peterson, Per A.
 TITLE OF INVENTION: PROTEIN GROWTH FACTOR FOR TREATING PROSTATE CANCER, AND RELATED
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Johnson & Johnson
 STREET: One J & J Plaza
 CITY: New Brunswick
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 08933
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/927,433

FILING DATE:
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Morrison, Alan J.
 REGISTRATION NUMBER: 37,399
 REFERENCE/DOCKET NUMBER: OPT-849
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 732-524-3592
 TELEFAX: 732-524-2808
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 112 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-927-433-7

Query Match 100.0%; Score 20; DB 3; Length 112;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
 DB 82 VLEP 85

Search completed: March 5, 2003, 08:34:35
 Job time : 15 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 5, 2003, 08:37:36, Search time 15 seconds
(without alignments)
25.636 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: RIQSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 86

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: PIP 73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	60.0	3	A33802	thyrotropin-releas
2	11	55.0	4	I51049	metallothionein-A
3	10	50.0	4	E44A23	synaptosomal assoc
4	8	40.0	4	A02147	phagocytosis-stimu
5	7	35.0	3	RHTD70	thyroliberin - Bom
6	7	35.0	3	RHPGT	thyroliberin - pig
7	7	35.0	3	RHSHT	thyroliberin - she
8	7	35.0	3	A92971	thyroliberin - eas
9	7	35.0	3	A43391	TRH-like tripeptid
10	7	35.0	3	A32971	tyrosine protein k
11	7	35.0	4	A32019	tyrosine melanocyt
12	7	35.0	4	P06140	carbon-monoxide de
13	7	35.0	4	A61300	22K superhelical D
14	7	35.0	4	I57745	D-mannosyl hydrol
15	7	35.0	4	S53508	saravation-induced
16	7	35.0	4	S17255	ribosomal protein
17	7	35.0	4	A14626	PPCH-related neuro
18	7	35.0	4	PT0740	lg heavy chain cnp
19	7	35.0	4	I54357	schwannomin - mous
20	7	35.0	4	PT0675	T-cell receptor be
21	6	30.0	4	A48360	gamma subunit of p
22	6	30.0	4	A77897	glucan 1,4-alpha-g
23	5	25.0	4	A41890	protein D - Escher
24	5	25.0	4	B43848	cell surface adhes
25	5	25.0	4	I40505	hypothetical prote
26	5	25.0	4	PT0677	T-cell receptor be
27	5	25.0	4	A56209	protein glutamine
28	5	25.0	4	S55238	palldipin - assas
29	4	20.0	3	P00010	angiotensin-conver

30	4	20.0	3	T13892	cytochrome c oxid
31	4	20.0	4	S18401	thyroglobulin - do
32	4	20.0	4	A37832	phorbol 12-myristate
33	4	20.0	4	I46627	hypothetical prote
34	4	20.0	4	S09478	globulin IV alpha
35	4	20.0	4	T20559	hypothetical prote
36	4	20.0	4	I38888	COL-1 inter 16 prot
37	4	20.0	4	A35775	sero-epitide Antio
38	4	20.0	4	A53284	T-cell receptor be
39	4	20.0	4	PT0445	T-cell receptor be
40	4	20.0	4	PT0721	T-cell receptor be
41	4	20.0	4	A40135	branched-chain ami
42	4	20.0	4	S47552	ubiquitin - rat
43	4	20.0	4	B23751	spinal cord peptid
44	3	15.0	3	B23751	histidinol dehydro
45	3	15.0	3	S13894	phosphatase C 1E
46	3	15.0	4	I40870	endoglucanase F
47	3	15.0	4	PT0271	lg heavy chain cnp
48	3	15.0	4	PT0633	T-cell receptor be
49	3	15.0	4	PT0551	T-cell receptor be
50	3	15.0	4	PT0697	T-cell receptor be

ALIGNMENTS

RESULT 1

A33802

thyrotropin-releasing hormone-like peptide - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 15-Jun-2001 #sequence_revision 15 Jun 2001 #text_change 15-Jun-2001

C:Accession: A33802

P:Coekle, S.M.; Aitken, A.J. Bc3, F.J. Smyth, D.G.

J. Biol. Chem. 264, 7788-7791, 1989

A:Title: A novel peptide, pyroglutamylglutamyproline amide, in the rabbit prostatic con

A:Reference number: A33802, WHIS 882101, P0107448405

A:Accession: A33802

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-3 <COC>

C:Superfamily: unassigned animal peptides

C:Keywords: amidated carboxyl end, pyroglutamic acid

F.1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

F.3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match: Similarity 60.0%, Score 12; DB 3; Length 3;

Best Local Similarity 100.0%, Pred No. 2.8e+05; Indels 0; Gaps 0;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4

DB 2 EP 3

RESULT 2

I51049

metallothionein-A - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 13-Sep-1994 #sequence_revision 13-Sep-1994 #text_change 21-Jul-2000

C:Accession: I51049

P:Olsson, P.E.; Fling, P.; Erkell, L.J.; Kille, P.

Eur. J. Biochem. 230, 344-349, 1995

A:Title: Structural and functional analysis of the rainbow trout (Oncorhynchus mykiss)

A:Reference number: I51049; M01D:35324545; M01D:7601121

A:Accession: I51049

A:Status: preliminary, translated from ORF/EMBL/CDDB

A:Molecule type: DNA

A:Residues: 1-4 <CDS>

A:Cross-references: EMBL:X80181; M01D:35324545; M01D:7601121

Query Match

Best Local Similarity 55.0%, Score 11; DB 2; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SEP 4
DB 1 MDP 3

RESULT 3

E44823
synaposomal-associated protein SNAP-25 peptide 1 - rabbit (fragment)
N/Alternate names: superprotein peptide 1
C/Species: *Oryctolagus cuniculus* (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18 Nov-1994 #text_change 15-Jun-1996
C/Accession: E44823
P/Cooley, A.; Liu, W.S.; Baittinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: A44823; MUID:92044785; PMID:1941090
A/Accession: E44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-4 <LOB>
A/Experimental source: visual tissue
A/Note: sequence extracted from NCBI backbone (NCBIP:64247)
C/Keywords: membrane trafficking

Query Match 50.0%; Score 10; DB 2; Length 4;
Best Local Similarity 33.3%; Pred No. 2.9e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 IME 3

RESULT 4

A02147
phagocytosis-stimulating peptide (tuftsin) - human
C/Species: *Homo sapiens* (man)
C/Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 01-Feb-1994
C/Accession: A02147
P/Mitchell, P.; Reinherz, E.L.; Satoh, F.S.; Najjar, V.A.
Biochem. Biophys. Res. Commun. 47, 172-179, 1972
A/Title: The characteristics, isolation and synthesis of the phagocytosis stimulating peptide
A/Reference number: A02147; MUID:70187993; PMID:4112763
A/Accession: A02147
A/Molecule type: protein
A/Residues: 1-4 <NIS>
A/Note: a peptide having the same structure, physical properties, and biological activity
P/Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3386-3392, 1967

A/Reference number: A77602; MUID:6001045; PMID:410272
A/Contents: annotation; immunoglobulin class
C/Comments: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils
n is essential for maximum stimulation of the phagocytic activity of neutrophils
C/Superfamily: immunoglobulin C region, immunoglobulin homology

Query Match 40.0%; Score 8; DB 2; Length 4;
Best Local Similarity 50.0%; Pred No. 2.9e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
DB 2 KP 3

RESULT 5

A02147

thyroliberin - *Bombina orientalis*
C/Species: *Bombina orientalis*
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A02147
P/Yasuhara, T.; Nakajima, T.
Chem. Pharm. Bull. 33, 2011-2013, 1975

A/Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A/Reference number: A90919; MUID:76114399; PMID:815011
A/Accession: A90919
A/Molecule type: protein
A/Residues: 1-3 <YAS>

C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid
P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
P3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No. 2.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

RESULT 6

RHPGT
thyroliberin - pig
C/Species: *Sus scrofa domestica* (domestic pig)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A01415
P/Nair, R.M.G.; Barrett, J.F.; Powers, C.V.; Schally, A.V.
Biochemistry 9, 1103-1106, 1970
A/Title: Structure of porcine thyrotropin releasing hormone.
A/Reference number: A05560; MUID:70136150; PMID:4984918
A/Accession: A01415
A/Molecule type: protein
A/Residues: 1-3 <NAI>

P/Poler, J.; Fournier, F.; Folkers, P.; Powers, C.V.; Schally, A.V.
Biochem. Biophys. Res. Commun. 37, 705-710, 1969
A/Title: The identity of chemical and hormonal properties of the thyrotropin releasing hormone
A/Reference number: A90167; MUID:70039904; PMID:4982117
A/Contents: annotation
A/Note: biological activities and P values (in 17 chromatographic systems) of the synthetic
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
P1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
P3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No. 2.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

RESULT 7

RHSHT
thyroliberin - sheep
C/Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A93750; A01415
P/Desiderio, J.; F.M.; Burgess, F.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 201-208, 1971

A/Title: The elucidation of the primary structure of the hypothalamic thyrotropin stimulating hormone
A/Reference number: A93750
A/Accession: A93750
A/Molecule type: protein
A/Residues: 1-3 <DES>
P/Burgess, F.; Dunn, T.F.; Desiderio, J.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 221-225, 1970
A/Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A/Reference number: A93750; MUID:70163386; PMID:4985794
A/Contents: annotation
A/Note: physicochemical characteristics and biological activities of the natural and synthetic
C/Superfamily: thyroliberin precursor
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No. 2.9e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 3 P 3

F1/Modified site: Pyroglutamic carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 3 P 3

RESULT 8

A:Title: thyroliberin - eastern newt (tentative sequence)
C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 15-Jun-2001 #sequence_revision 15 Jun-2001 #text_change 15 Jun-2001
C:Accession: A02971; A01415
P:Grimm-Jorgensen, Y.; McKelvey, J.F.
J. Neurochem. 23, 471-478, 1974
A:Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain
A:Reference number: A02971; MUIP-75035605; PMID:4214538
A:Accession: A02971
A:Molecule type: protein
A:Residues: 1-3 <GR1>
A:Note: a peptide with the chemoattractant and electrophoretic characteristics of thyroliberin, or glutamic acid
C:Superfamily: thyroliberin precursor
F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 3 P 3

RESULT 9

A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamic acid (Gln) #status experimental
C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15 Jun-2001
C:Accession: A43391
R:Lackey, D.B. 267, 17508-17511, 1992
J. Biol. Chem.

A:Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroglutamic acid (Gln) #status experimental
C:Species: Medicago sativa (alfalfa)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15 Jun-2001
C:Accession: A43391
A:Molecule type: protein
A:Residues: 1-3 <LAC>
F1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental
F3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 3 P 3

RESULT 10

A:Title: tyrosine protein kinase - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C:Accession: I78890

F:Chow, R.M.; Davidson, E.; Farnell, M.; Gosselin, E.; Lemire, S.; Lys, M.; Pozak, J.
Oncogene 9, 3437-3448, 1994
A:Title: Two distinct protein isoforms are encoded by ptk, a c-kit related tyrosine protein kinase
A:Reference number: I64497; MUIP-66666666; PMID:7670703
A:Accession: I78890
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-3 <RES>
A:Cross-references: GB:L33339, NID:G609516, FIDN:AAA64432.1; PID:G609516
C:Genetics:
A:Gene: p52ntk

Query Match 35.0%; Score 7; DB 3; Length 3;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 2 P 2

RESULT 11

A:Title: tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 (bovine)
C:Species: Bos primigenius taurus (cattle)
C:Date: 15-Jul-1993 #sequence_revision 11 Jul 1993 #text_change 14-Aug-2000
C:Accession: A32039
R:Horvath, A.; Kastin, A.J.
J. Biol. Chem. 268, 2175-2179, 1993
A:Title: Isolation of tyrosine melanocyte-stimulating hormone release-inhibiting factor 1 (bovine)
A:Reference number: A32039; MUIP-94123245; PMID:12563371
A:Accession: A32039
A:Molecule type: protein
A:Residues: 1-4 <HOR>
A:Experimental source: brain
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end
F1/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 2 P 2

RESULT 12

A:Title: carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain. Pseudomonas aeruginosa
C:Species: Pseudomonas carboxydohydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C:Accession: P01140
R:Kraut, M.; Hagedieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Heterology and distribution of carbon monoxide dehydrogenase gene in the tyrosine
A:Reference number: P01140; MUIP-90055674; PMID:2418128
A:Accession: P01140
A:Molecule type: protein
A:Residues: 1-4 <KRA>
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, and small

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred No 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
|
DB 4 P 4

RESULT 13

A61300
2X superhelical DNA binding protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
C:Accession: A61300
R:Kishi, F.; Elina, Y.; Miki, T.; Nakazawa, T.; Nakazawa, A.
J. Biochem. 92, 1059-1068, 1982
A:Title: Purification and characterization of a protein from Escherichia coli which forms a DNA-protein complex
A:Reference number: A61300; PMID:8468496; PMID:6294062
A:Accession: A61300
A:Molecule type: protein
A:Residues: 1-4 <KIS>
A:Comment: This protein resembles some of the histone-like protein of bacteria in amino acid composition
C:Keywords: DNA binding, monomer

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
DB 1 ME 2

RESULT 14

157745
D-mannanase hydrolase (uxuA) - Escherichia coli
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
C:Accession: 157745
R:Blanco, C.; Ritzenthaler, F.; Kolt, A.
Mol. Gen. Genet. 262, 112-119, 1986
A:Title: The regulatory region of the uxuA operon in Escherichia coli K12
A:Reference number: 157745; PMID:86374344; PMID:3083215
A:Accession: 157745
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-4 <EE>
A:Cross-references: EMBL X03411; NID 943309; PDB 0XAC147 1; FID:9581954

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
DB 1 ME 2

RESULT 15

S53508
starvation-induced ribonuclease - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 07-May-1999
C:Accession: S53508
R:Koeck, M.; Loeffler, A.; Abel, S.; Glund, K.
Plant Mol. Biol. 27, 477-485, 1995
A:Title: cDNA structure and regulatory properties of a family of starvation-induced ribonucleases
A:Reference number: S53506; PMID:9520142; PMID:7934213
A:Accession: S53508
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <KE>

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 2 F 2

RESULT 16

S17255
ribosomal protein Yml1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae)
C:Species: Saccharomyces cerevisiae
C:Variety: strain 07173
C:Date: 23-Apr-1991 #sequence_revision 14-Sep-1994 #text_change 09-May-1997
C:Accession: S17255
R:Grohmann, L.; Graack, H.P.; Kruff, V.; Choli, T.; Goldschmidt-Reisin, S.; Kitakawa, M.
FEBS Lett. 294, 51-56, 1991
A:Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast
A:Reference number: S17255; PMID:2381107; PMID:2560426
A:Accession: S17255
A:Molecule type: protein
A:Residues: 1-4 <EPQ>
A:Comment: A coding region for this protein could not be identified in the genome of Saccharomyces cerevisiae
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 4 P 4

RESULT 17

A34626
RPM1-related neurotrophin - ferruginous spindle
C:Species: Fusinus ferrugineus (ferruginous spindle)
C:Date: 02-Jul-1992 #sequence_revision 02-Jul-1992 #text_change 11-Dec-1993
C:Accession: A34626
R:Kobayashi, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.
Biochem. Biophys. Res. Commun. 187, 773-779, 1990
A:Title: A molluscan neurotrophin related to the crustacean hormone, RPCH
A:Reference number: A34626; PMID:20179762; PMID:2310194
A:Accession: A34626
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-4 <ROP>
C:Keywords: neurotrophin

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
DB 2 P 2

RESULT 18

PT0240
Ig heavy chain CDR3 region (clone 2-100B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1993 #sequence_revision 20-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0240
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Garon, A.J.; Povera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and joining segments in the CDR3 region of human Ig heavy chain CDR3
A:Reference number: PT0240; PMID:91108327; PMID:1899102
A:Accession: PT0240
A:Molecule type: DNA
A:Residues: 1-4 <YAM>
A:Experimental source: R lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 35.0%; Score 7; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2 8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A.Pesidues: 1-4 <CAP>
 A.Cross-references: GB 891987; MID:G454213; PID:AB21391.1; PID:G245214
 A.Note: Sequence extracted from NFB1 backbone (NFB1-1999; NFB1P181912)

Query Match 30.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred No. 2 8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
 |
 Db 2 LQ 3

RESULT 22

A7897
 Glycan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus phoenicis (fragment)
 N.Alternate names: glucamylase
 C.Species: Aspergillus phoenicis
 C.Date: 16-Aug-1988 #sequence_revision 16 Aug-1988 #text_change 06-Jul-1996
 C.Accession: A27897
 R.Inokuchi, N.; Takahashi, T.; Irie, M.
 J. Biochem. 90, 1055-1067, 1991
 A.Title: Purification and characterization of a major glucamylase from Aspergillus niger

A.Reference number: A27897; MID:82075730; PMID:6796572
 A.Note: Aspergillus saitoi
 A.Accession: A27897
 A.Molecule type: protein
 A.Residues: 1-4 <INO>
 C.Keywords: Glycosidase, hydrolase, polysaccharide degradation

Query Match 30.0%; Score 6; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred No. 2 8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
 |
 Db 2 VI 3

RESULT 23

A1890
 protein D - Escherichia coli (fragment)

C.Species: Escherichia coli
 C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C.Accession: A41890
 R.Slettan, A.; Gebhardt, K.; Kristiansen, E.; Birkeland, N.K.; Lindquist, B.H.
 J. Bacteriol. 174, 4094-4100, 1992
 A.Title: Escherichia coli P 12 and B contain functional heat-labile P-12 and B

A.Reference number: A41890; MID:92283767; PMID:1597424
 A.Accession: A41890
 A.Status: preliminary
 A.Molecule type: DNA
 A.Pesidues: 1-4 <SLE>
 A.Cross-references: GB:M81463

Query Match 25.0%; Score 5; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred No. 2 8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3
 |
 Db 1 E 1

RESULT 24

B43848

Cell surface adhesin for heparan sulfate, CCK Staphylococcus aureus (fragment)
 C.Species: Staphylococcus aureus
 C.Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1996
 C.Accession: B43848
 R.Liang, C.P.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.
 Infect Immun. 60, 899-906, 1992
 A.Title: Binding of heparan sulfate to Staphylococcus aureus.

QY 4 P 4
 |
 Db 2 P 2

RESULT 19

I54357
 schwannomin - mouse (fragment)
 C.Species: Mus musculus (house mouse)
 C.Date: 02-Aug-1994 #sequence_revision 02 Aug-1994 #text_change 05-Nov-1999
 C.Accession: I54357
 R.Huyth, D.P.; Nechiporuk, T.; Pulst, S.
 Hum. Mol. Genet. 3, 1075-1079, 1994

A.Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co-expressed with the NF2 gene
 A.Reference number: I54357; MID:95072570; PMID:7991675
 A.Accession: I54357
 A.Status: preliminary; translated from cDNA/EMBL/GenBank
 A.Molecule type: mRNA
 A.Residues: 1-4 <RES>
 A.Cross-references: GB:138848; MID:G454496; PID:AAA67160.1; PID:G601923
 C.Genetics:
 A.Gene: NF2

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred No. 2 8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
 |
 Db 2 P 2

RESULT 20

PT0675
 T-cell receptor beta chain V D-J region (140-14C) - mouse (fragment)

C.Species: Mus musculus (house mouse)
 C.Date: 17-Jul-1992 #sequence_revision 17 Jul-1992 #text_change 30-May-1997
 C.Accession: PT0675
 R.Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991
 A.Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A.Reference number: PT0675; MID:91277601; PMID:1711564

A.Accession: PT0675
 A.Status: translation not shown
 A.Molecule type: DNA
 A.Residues: 1-4 <PEE>

A.Experimental source: day 14 fetal thymus, strain BA.12/-
 C.Keywords: T-cell receptor

Query Match 35.0%; Score 7; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred No. 2 8e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 P 4
 |
 Db 4 P 4

RESULT 21

A48360
 gamma subunit of Protein A - Methylosinus trichosporium (fragment)

C.Species: Methylosinus trichosporium
 C.Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
 C.Accession: A48360
 P.Cady, D.L.; Laidler, V.; Salmond, J.P.; Murrell, J.C.

Arch. Microbiol. 156, 477-481, 1991
 A.Title: The methane monooxygenase gene cluster of Methylosinus trichosporium: cloning a

A.Reference number: A48360; MID:92161811; PMID:1787094
 A.Contents: OB3b
 A.Accession: A48360
 A.Status: preliminary
 A.Molecule type: DNA

A:Reference number: A43848; MUID:92176005; PMID:1541563

A:Accession: B43848

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-4 <LIA>

A>Note: sequence extracted from NCBI: backbone (NCBIP.85444)

Query Match 25.0%; Score 5; DB 2; Length 4;
Best Local Similarity 50.0%; Pred No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
:
DB 1 ML 2

RESULT 25

140505

hypothetical protein 3 (4 aa) - Bacillus stearothermophilus

C:Species: Bacillus stearothermophilus

C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999

C:Accession: 140505

P:Waye, M M ; Winter, G

Eur. J. Biochem. 188, 505-510, 1986

A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synthetase gene of Bacillus stearothermophilus

A:Reference number: 140505; MUID:86074732; PMID:3522162

A:Accession: 140505

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-4 <RES>

A:Cross-references EMBL X04193; NID:G40233; FIDN:GAA07793.1; PID:G580944

Query Match 25.0%; Score 5; DB 2; Length 4;
Best Local Similarity 50.0%; Pred No. 2.8e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VL 2
:
DB 1 ML 2

Search completed: March 5, 2003, 08:40:49
Job time : 16 secs

CC (AND OTHER TISSUES) DURING HYPERSENSITIVITY REACTIONS
 CC (ANAPHYLAXIS) THEIR ACTIVITIES, PREPOTENTIALLY AFFECTING
 CC EOSINOPHILS, INCLUDE CHEMOTAXIS, CHEMOTACTIC DEACTIVATION, RELEASE
 CC OF ENZYMES, AND STIMULATION OF THE HEXOSE MONOPHOSPHATE SHUNT.
 DR PIR; A03190; ETHL.

FT VARIANT 1 V -> A (IN OTHER PEPTIDE)
 FT MOD_RES 1 /FTID=VAP_005201
 SQ SEQUENCE 4 AA; 598 MW; 69058962A00000000 CRC64;

Query Match 25.0%; Score 5; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred No 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 E 3
 DB 4 E 4

RESULT 6

FLRF_HIRME STANDARD; PRT; 4 AA.

AC P42562;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide YLRP-amide.
 OS Hirudo medicinalis [Medicinal leech].
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinoi;
 OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo
 OX NCBI_TaxID=6421;
 RN [1]

RP SEQUENCE.
 RX MEDLINE=92195954; PubMed=1686933;
 RA Evans R D., Pohl J., Kartsonis M A., Calabrese P L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 CC -1- SIMILARITY BELONGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.

KW Neuropeptide; Amidation.
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 4 AA; 598 MW; 6904071B300000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred No 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
 DB 2 L 2

RESULT 7

FLRF_HIRME STANDARD; PRT; 4 AA.

AC P42561;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FLRFamide.
 OS Hirudo medicinalis [Medicinal leech], and
 OS Helisoma trivolvis [Shall].
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea, Hirudinoi;
 OC Arynchobdellida; Hirudiniiformes; Hirudinidae; Hirudo.
 OX NCBI_TaxID=6421, 27815;
 RN [1]

RP SEQUENCE.

EX MEDLINE=92195954; PubMed=1686933;
 RA Evans R D., Pohl J., Kartsonis M A., Calabrese P L.;
 RT "Identification of RFamide neuropeptides in the medicinal leech."
 RL Peptides 12:897-908(1991).
 RN [2]

RP SEQUENCE

PC SPECIES=H. trivolvis; TISSUE=Kidney;
 EX MEDLINE 94286417; PubMed=7942409;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.P., Salomadin A.S.M.;
 RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
 trivolvis."
 RL Peptides 15:31-36(1994)
 CC -1- SIMILARITY BELONGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 4 AA; 582 MW; 64F4072A00000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred No 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
 DB 2 L 2

RESULT 8

FLRF_ANTEL STANDARD; PRT; 4 AA.

AC P58707;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Antho-PNamide.
 OS Anthopleura elegantissima (Sea anemone).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
 OC Nynanthaea; Actiniidae; Anthopleura.
 OX NCBI_TaxID=6110;

RP SEQUENCE, AND MASS-SPECTROMETRY.

EX MEDLINE=90316722; PubMed=1973545;
 RA Grimmelikhuijzen C.J.P., Pinehart K.L. Jr., Jacob E., Graff D.,
 RA Peinscheid P.K., Northacker H.-P., Staley A.L.;
 RT "Isolation of L-3-Phenylactyl-Lys-Arg-Asp-NH₂ (Antho-PNamide), a sea
 anemone neuropeptide containing an unusual amino-terminal blocking
 group."
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).

CC -1- SURCELLULAR LOCATION. Secreted.
 CC -1- TISSUE SPECIFICITY. Neuron-specific.

CZ -1- MASS SPECTROMETRY MW 549.3, METHOD=D=FAH.

KW Neuropeptide; Amidation.
 FT MOD_RES 1
 FT MOD_RES 1
 FT MOD_RES 4
 FT MOD_RES 4
 SQ SEQUENCE 4 AA; 549 MW; 64F4072A00000000 CRC64;

Query Match 20.0%; Score 4; DB 1; Length 4;
 Best Local Similarity 100.0%; Pred No 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 L 2
 DB 2 L 2

RESULT 9

LUKE_VIBFI STANDARD; PRT; 3 AA.

AC P24272;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Long-chain-fatty-acid-luciferin-component ligase (EC 6.2.1.19) (Acy-
 DE protein synthetase) (Fragment).
 GN LUKE.

OS Vibrio fischeri.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrion-
 OX NCBI_TaxID=668;

RN [1]


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ID DCMS_PSECH STANDARD: PRT: 4 AA.
AC P19918:
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit S) (CO-DH S) (Fragment).
GN CUTS.
OS Pseudomonas carboxydohydrogena
OC Bacteria: Proteobacteria; alpha subdivision; Rhodospirillaceae group;
OC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055679; PubMed=2918128;
RA Kraut M., Hupendieck I., Horwig S., Meyer O.;
PT "Homology and distribution of CO dehydrogenase structural genes in
PT carboxydohydrogenic bacteria.";
FT Arch. Microbiol. 152:135-141(1990)
RL Arch. Microbiol. 152:135-141(1990)
CC - - - FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC - - - CATALYTIC ACTIVITY: CO + H2O + acceptor = CO2 + reduced
CC acceptor.
CC - - - COFACTOR: RIMS TWO ZINC-ION CLUSTERS
CC - - - SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; P01146; P01146.
KW Oxidoreductase; Iron-sulfur.
FT NON_TER 4
SQ SEQUENCE 4 AA: 420 MW: 6003006600000000 CPC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred No 1 le:05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 L 2
DB 1 M 1

RESULT 13
FAR4_HIRME
ID FAR4_HIRME STANDARD: PRT: 4 AA.
AC P42563;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 01-NOV-1995 (rel. 32, Last annotation update)
DE FMRFamide-like neuropeptide YMPF-amide
OS Hirudo medicinalis (Medicinal leech)
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinina;
OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
OX NCBI_TaxID=6421;
RN [1]
RP SEQUENCE
RX MEDLINE=92195954; PubMed=1686933;
RA Evans R.D., Pohl J., Karsonis M.A., Calabrese P.L.;
RT "Identification of Pheamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC - - - SIMILARITY: RELATINGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA: 616 MW: 6040688300000000 CPC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred No 1 le:05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 L 2
DB 2 M 2

```

```

RESULT 14
FMRF MACNI
ID FMRF MACNI STANDARD: PRT: 4 AA.
AC P01162;
DT 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUN-1998 (rel. 36, Last annotation update)
DE FMRFamide (Peak C) (Cardioexcitatory neuropeptide).
OS Macrocallista nimbosa (Sun-ray clam),
OS Nereis virens (Sandworm),
OS Hirudo medicinalis (Medicinal leech), and
OS Helisoma trivolvis (Snail).
OC Eukaryota; Metazoa; Mollusca; Rivalvia; Heterobranchia; Veneroida;
OC Veneroidea; Veneridae; Macrocallista.
OX NCBI_TaxID=6594, 6353, 6421, 27815;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RX SPECIES=M.nimbosa, TISSUE=Cerebral pedal, and Visceral ganglion;
RX MEDLINE=77215956; PubMed=877582;
RA Price D.A., Greenberg M.J.;
RT "Structure of a molluscan cardioexcitatory neuropeptide.";
RL Science 197:670-671(1977).
RN [2]
RP SEQUENCE, AND CHARACTERIZATION.
RX SPECIES=M.nimbosa, TISSUE=Ganglion;
RX MEDLINE=78012038; PubMed=909875;
RA Price D.A., Greenberg M.J.;
RT "Purification and characterization of a cardioexcitatory neuropeptide
RT from the central ganglia of a bivalve mollusc.";
RL Prep. Biochem. 7:261-261(1977)
RN [3]
RP SEQUENCE.
RX SPECIES=N.virens,
RX MEDLINE=92259866; PubMed=2342992;
RA Krajinak K.G., Price D.A.;
RT "Authentic FMRFamide is present in the polychaete Nereis virens.";
RL Peptides 11:75-77(1990)
RN [4]
RP SEQUENCE.
RX SPECIES=H.medicalis;
RX MEDLINE=92195954; PubMed=1686933;
RA Evans R.D., Pohl J., Karsonis M.A., Calabrese P.L.;
RT "Identification of Pheamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
RN [5]
RP SEQUENCE
RX SPECIES=H.trivolvis, TISSUE=Kidney;
RX MEDLINE=94286417; PubMed=7913438;
RA Madrid F.P., Price D.A., Greenberg M.J., Phan H.P., Calabrese P.L.;
RT "FMRFamide-related peptides from the kidney of the snail, Helisoma
RT trivolvis.";
RL Peptides 15:31-36(1994).
CC - - - FUNCTION: MYOACTIVE; CARDIOEXCITATORY SUBSTANCE. PHARMACOLOGICAL
CC ACTIVITIES INCLUDE ACCELERATION, INDUCTION, AND REGULATION OF
CC CARDIAC CONTRACTION.
CC - - - SIMILARITY: RELATINGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR; A01426; ECNK.
DR PIR; A60418; A60418.
KW Neuropeptide; Amidation.
FT MOD_RES 4
SQ SEQUENCE 4 AA: 600 MW: 6504069400000000 CPC64;

Query Match 10.0%; Score 2; DB 1; Length 4;
Best Local Similarity 0.0%; Pred No 1 le:05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 L 2
DB 2 M 2

```

RESULT 15

OCPI OCTMI
ID OCPI OCTMI STANDARD, PRT, 4 AA.
AC P58648;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Eukaryota, Metazoa, Mollusca, Cephalopoda, Colecoidea, Octopoda;
OC Inciliata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RS SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION
KA TISSUE=Brain;
RX MEDLINE=20336915; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.,
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-2 is a 1000 time less
active than Ocp-1.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-2 has 1 Phe instead of D-Phe.
CC -!- MASS SPECTROMETRY: MW=435.2, METH-C-MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA, 394 MW, 6AA879C816C0C0C0C CRC64;

Query Match 10.0%; Score 2; DB 1, Length 4,
Best Local Similarity 0.0%; Pred.No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3
DB 4 D 4

RESULT 16
OCPI OCTMI
ID OCPI OCTMI STANDARD, PRT, 4 AA.
AC P58649;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Eukaryota, Metazoa, Mollusca, Cephalopoda, Colecoidea, Octopoda;
OC Inciliata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RS SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
KA TISSUE=Brain;
RX MEDLINE=20336915; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.,
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
Octopus minor";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
inotropic effects on the heart. Ocp-4 is a 1000 time less
active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2, VETHCD-MALDI.
KW Hormone; D-amino acid.
FT MOD_RES 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA, 463 MW, 6AR3E58A16A0A0A0C CRC64;

Query Match 10.0%; Score 2; DB 1, Length 4;
Best Local Similarity 0.0%; Pred.No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3

DB 4 D 4
RESULT 17
GRWM HUMAN
ID GRWM HUMAN STANDARD, PRT, 3 AA.
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human).
OC Eukaryota, Metazoa, Chordata, Vertebrata; Pyraloecetomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE.
FX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.,
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine";
RL Experientia 33:324-325(1977).
CC -!- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DE PIF, A01421; OPHI
SQ SEQUENCE 3 AA, 346 MW, 6311E1A1000000000 CRC64;

Query Match 5.0%; Score 1; DB 1, Length 3;
Best Local Similarity 0.0%; Pred.No. 1.1e+05;
Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3
DB 3 K 3

RESULT 18
FFKA ANTEL
ID FFKA ANTEL STANDARD, PRT, 4 AA.
AC P58705;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-KAamide
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota, Metazoa, Cnidaria, Anthozoa; Zoantharia; Actiniaria;
OC Pycnantheae; Actiniidae; Anthopleura.
OX NCBI_TaxID=6110,
RN [1]
RS SEQUENCE.
RX MEDLINE=92028952; PubMed=1691803;
PA McFarlane J.P., Finehart K.L. Jr., Grimmelikhuizen C.J.P.,
RT "Isolation of L-3 phenylacetyl-Phe-Lys Ala-NH2 (Antho-KAamide), a
novel neuropeptide from sea anemones";
EL Biochem Biophys Res Commun 179:1205-1211(1991).
RN [2]
RS FUNCTION.
PX MEDLINE=93301436; PubMed=8397415;
PA McFarlane J.P., Hudson D., McFarlane H.P., Grimmelikhuizen C.J.P.,
RT "The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-KAamide and Antho-Ramide";
FL Proc P Soc Lond B Biol Sci 362:183-189(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
behaviour in sea anemones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuronal specific.
KW Neuropeptide; Amidation.
FT MOD_RES 1 L-3-PHENYLACETYL-
FT MOD_RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA, 512 MW, 6DE13A7A0A0A0A0A0C CRC64;

Query Match 5.0%; Score 1; DB 1, Length 4;

Best Local Similarity 0.0%; Pred No 1 le-05;
Matches a; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 E 3
Db 3 K 3

Search completed: March 5, 2003, 08:38:49
Job time : 11 secs



Genome version 5.1.3
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OM protein protein search, using sw model

Run on: March 5, 2003, 08:37:06 ; Search time 92 Seconds
(without alignments)
8 459 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20

Sequence: 1 VLEP 4

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 286047115 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvivirus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	45.0	4	11 Q08433	Q08433 rattus norv

ALIGNMENTS

RESULT 1
Q08433
ID Q08433 PRELIMINARY; PRT; 4 AA.
AC Q08433;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01 JAN 1999 (TREMBLrel. 09, Last annotation update)
DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)
(Fragment).
OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC RNS_13775-13116,
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GUNN;
PA MEDLINE=91282758; PubMed=1840486;
PA Sato H., Aono S., Fashiwamara S., Yoiwai O.;
PT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the
PL hyperbilirubinemic Gunn rat.", 177-1164 (1991).
CC R Biochem Biophys Res Commun 177:1161-1164 (1991).
CC -!- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND
CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND
CC ENDOGENOUS COMPOUNDS.
CC -!- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR -> UDP + ACCEPTEP
CC -!- PETA-D-GLUCOPONOSIDE.
CC -!- SUBCELLULAR LOCATION: MICROsome.
DR EMBL; S38636; AAB19259.1; .
KW Transferase; Glycosyltransferase; Microsome; Multigene family.
FT NON_TER 1 1
FT NON_TER 4 4
SQ SEQUENCE 4 AA; 473 MW; 5337320420000000000 CFC64;
Query Match 45.0%; Score 9; DB 11; Length 4;
Best Local Similarity 66.7%; Pred No. 6.7e+04;
Matches 2; Conservative 1; Mismatches 0; Gaps 0;
QY 1 VLE 3
DB 2 VLE 4

Search completed: March 5, 2003, 08:40:27

Job time : 93 secs

OM protein - protein search, using sw model

Run on: March 5, 2003, 08:34:20, Search time 33 seconds
(without alignments)
16.152 Million cell updates/sec

Title: US-09-732 411-15

Perfect score: 20

Sequence: 1 VLRP 4

Scoring table: BLASTNM62

Gapop: 10.0, Gapext: 0.5

Searched: 90470 seqs, 13250620 residues

Total number of hits satisfying chosen parameters: 11315

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: A: Geneseq.j01002.*

	1:	2:	3:	4:	5:	6:	7:	8:	9:	10:	11:	12:	13:	14:	15:	16:	17:	18:	19:	20:	21:	22:	23:
	/SID22/qcgdata/geneseq/geneseq-emb1/AA1980.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1981.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1982.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1983.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1984.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1985.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1986.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1987.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1988.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1989.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1990.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1991.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1992.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1993.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1994.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1995.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1996.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1997.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1998.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA1999.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA2000.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA2001.DAT.*	/SID22/qcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	4	21	Chemotactic peptide
2	20	100.0	4	22	Adhesion-modulator
3	16	80.0	4	20	Interleukin 1 beta
4	14	70.0	4	20	Peptide used to ma
5	14	70.0	4	21	Chemotactic peptide
6	14	70.0	4	21	Granzyme B substra
7	14	70.0	4	21	Granzyme B substra
8	14	70.0	4	22	Fluorophore-label
9	14	70.0	4	22	Chicken bone deriv
10	14	70.0	4	22	Granzyme B peptide

11	14	70.0	4	22	AAG62501
12	14	70.0	4	22	AAP29759
13	14	70.0	4	23	Escherichia coli r
14	14	70.0	4	23	Granzyme B peptide
15	14	70.0	4	23	Tumour associated
16	14	70.0	4	23	Tumour associated
17	14	70.0	4	23	Tumour associated
18	14	70.0	4	23	Tumour associated
19	13	65.0	4	8	Immunomodulator pe
20	13	65.0	4	13	ATP inhibitor pep
21	13	65.0	4	16	Antineoplastic pep
22	13	65.0	4	19	Human erythropoiet
23	13	65.0	4	20	Peptide used to ma
24	13	65.0	4	20	Human growth hormo
25	13	65.0	4	20	Human growth hormo
26	13	65.0	4	21	Fluorophore-label
27	13	65.0	4	21	Cathepsin B coll ad
28	13	65.0	4	22	Chicken bone deriv
29	13	65.0	4	22	Peptide which is u
30	12	60.0	4	23	Thyrotropin releas
31	12	60.0	2	22	Thyrotropin releas
32	12	60.0	3	16	Tripeptide having
33	12	60.0	3	19	Anti-inflammatory
34	12	60.0	3	21	Peptide used as an
35	12	60.0	4	5	Animal growth prom
36	12	60.0	4	5	Animal growth prom
37	12	60.0	4	9	Acetylcholinestera
38	12	60.0	4	9	Sequence of peptide
39	12	60.0	4	14	Diuretic hormone b
40	12	60.0	4	14	Diuretic hormone b
41	12	60.0	4	14	Diuretic hormone d
42	12	60.0	4	15	Diuretic hormone d
43	12	60.0	4	16	Oligopeptide deriv
44	12	60.0	4	16	Human growth hormo
45	12	60.0	4	16	Oligopeptide deriv
46	12	60.0	4	16	Immunostimulating
47	12	60.0	4	16	Tetrapeptide deriv
48	12	60.0	4	16	Tetrapeptide deriv
49	12	60.0	4	16	Peptide binding to
50	12	60.0	4	16	Peptidase substrat

ALIGNMENTS

RESULT 1

AA828663
ID AA828663 standard; peptide; 4 AA.

XX AA828663;

XX 13-PEB-2001 (first entry)

XX Chemotactic peptide pepJ'

XX Chemotactic; osteopontin; vulnery; antiarthritic; antipruritic;
KW cytostatic; antitumor; antiinflammatory; osteopathic;
KW wound healing; cell migration; chemotaxis; atherosclerosis; cancer;
KW angiogenic-associated disease; arthritis; psoriasis; haemangioma;
KW ocular neovascularisation; cell apoptosis; nitrous oxide production;
KW inflammation; osteoporosis; immune disease.

XX Mammalia.

XX Synthetic.

XX WC290902247 A2.

XX Peptide used to ma

XX Chemotactic peptide

XX Granzyme B substra

XX 17-APP-2000; 2000WO-US10344.

XX 15-APP-1999; 99US-0129764.

XX

PA (CHIL-) CHILDRENS MEDICAL CENT.
 XX Ashkar S;
 XX WPI: 2000-007109/47
 XX
 XX New osteopontin-derived chemotactic and inhibitory peptides, useful for
 PT preventing scarless wound healing, modulating cellular chemotaxis,
 PT treating formation of atherosclerotic plaques and preventing metastasis
 PT
 XX
 XX Claim 17; Page 43; 54pp; English.
 PS
 XX The present sequence is an osteopontin-derived chemotactic peptide.
 CC Such chemotactic peptides are useful for promoting scarless wound
 CC healing, modulating chemotaxis and promoting cell migration to a target
 CC site in a cell of a subject. They are also used for modulating cellular
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
 CC useful for treating the formation of atherosclerotic plaques in a
 CC subject. The peptides are used for preventing metastasis, treating an
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
 CC tumour metastasis or ocular neovascularisation. They are also used for
 CC activating cell apoptosis, for modulating nitrous oxide production and
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune
 CC diseases. They can also be used to enhance an immune response by
 CC attracting macrophages.
 XX
 XX Sequence 4 AA;
 SQ
 Query Match 100.0%; Score 20; DE 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7 Re+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 Db ||||
 1 VLEP 4
 RESULT 2
 AAB29558
 ID AAB29558 standard; peptide; 4 AA.
 XX
 XX AAB29558;
 AC
 XX
 XX 14-FEB-2001 (first entry)
 DT
 XX
 XX Adhesion-modulatory peptide, SEQ ID NO:15.
 DE
 XX Adhesion modulatory peptide; target cell adhesion; cell adhesion;
 KW endothelial cell; fibroblast; macrophage; neutrophil; myofibroblast;
 KW collagen; glycosaminoglycan; extracellular matrix; synthetic substrate;
 KW vascular growth; wound healing; keloid formation; scarring; fibrosis;
 KW anti-infective; vulvar; immunomodulatory; antibacterial; anticancer;
 KW anti-tumorigenic; anti CD44 activity; prostheses; implants.
 XX
 XX Synthetic.
 OS
 XX W0200006324-A2
 PN
 XX
 XX 26-QRT-2000
 PD
 XX
 XX 17-APP-2000; 2000WO US10329.
 PF
 XX
 XX 16-APP-1999; 99US-0129709.
 PP
 XX
 XX (CHIL-) CHILDRENS MEDICAL CENT
 PA
 XX Ashkar S;
 PI
 XX WPI: 2001-007002/01
 DR
 XX

PT Novel adhesive modulatory peptides useful for modulating adhesion of
 PT target cells such as endothelial cells, fibroblasts, macrophages to
 PT substrate such as polyvinyl surfaces, collagen
 XX
 XX Claim 8; Page 27; 35pp; English.
 PS
 XX The invention relates to novel adhesion modulatory peptides (AAB29544-
 CC AAB29558) which modulate the adhesion of a target cell to a substrate.
 CC The invention also encompasses substrates and devices treated with a
 CC peptide of the invention; compositions comprising a peptide of the
 CC invention for in vivo use; and analogues, fragments and chemical
 CC derivatives of the peptides of the invention. The peptides are useful for
 CC modulating the adhesion to a substrate of target cells such as
 CC endothelial cells, fibroblasts, macrophages, neutrophils or
 CC myofibroblasts. The substrate may be a substrate that is found in the
 CC body of a patient, e.g., collagen or hyaluronic acid, or may be a
 CC synthetic substrate e.g., a polyvinyl surface, titanium or PGA. The
 CC peptides are useful for regulating vessel growth during wound healing
 CC and/or in the treatment of damage resulting from vascular disease; for
 CC inhibiting or preventing cellular apoptosis; in the treatment of
 CC fibrosis, in particular in the clearing of debris; to minimise wound
 CC contraction, thereby reducing keloid tissue formation and scarring; and
 CC as anti clotting agents. The peptides also have an immunomodulatory
 CC effect, and an antibacterial effect by adhering to neutrophils.
 CC Additionally, peptides of the invention have an anticancer effect by
 CC competing for alpha-v-beta3 integrin binding on the cell surface, and an
 CC antitumorigenic effect by having anti-CD44 activity. The peptides are
 CC useful for stimulating and/or enhancing cell attachment to polymer
 CC scaffolds, to enhance tissue growth and for coating medical devices,
 CC including prostheses and implants (e.g., vascular implants). The present
 CC sequence represents a specifically claimed adhesion modulatory peptide of
 CC the invention.
 XX
 XX Sequence 4 AA,
 SQ
 Query Match 100.0%; Score 20; DE 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLEP 4
 Db ||||
 1 VLEP 4
 RESULT 3
 AAY03962
 ID AAY03962 standard; peptide; 4 AA.
 XX
 XX AAY03962;
 AC
 XX
 XX 23-JUN-1999 (first entry)
 DT
 XX Interleukin-1 beta converting enzyme binding moiety.
 DE
 XX Cysteine protease inhibitor; exadiarole, thiadiazole, 1,2,4 triazole;
 KW interleukin-1 beta converting enzyme inhibitor; IL-1; ICE; anti-tumor;
 KW anticancer; antimicrobial; antibacterial; antiviral; anti-allergic;
 KW anti-inflammatory; herbicide; fungicide; pesticide; multiple sclerosis;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW ischaemic-reperfusion injury.
 XX
 XX Synthetic.
 OS
 XX WC9849190 A2.
 PN
 XX
 XX 05-NOV-1998.
 PD
 XX
 XX 24-APP-1998; 98WO-US08259
 PP
 XX
 XX 23-APP-1998; 98US-0044819
 PF
 XX
 XX 25-APP-1997; 97US-0044819.
 PP
 XX (COPT-) COPT-TECH INC.
 PA

XX Cheronis Jⁿ, Gerrity Hⁿ, Goodfellow VS, Gyorkos AC;
 PI Leimer AH, Spruce LW, Young JM;
 XX WPI; 1999-131683/11.
 XX New substituted oxadiazole cysteine protease inhibitors - useful
 PT e.g. for inhibiting cancer cell growth, microbial cell or viral
 PT growth or treating inflammatory and degenerative diseases
 XX
 PS Claims 61, 62; Pages 67, 68; 82pp; English.
 XX New compounds are presented which consist of a cysteine protease
 CC binding moiety attached by its C-terminal to an oxadiazole, thiadiazole
 CC or 1,2,4 triazole moiety. These compounds are cysteine protease
 CC inhibitors useful for inhibiting the enzymatic activity of calpain,
 CC cathepsin, caspase (e.g. human interleukin-1 beta converting enzyme),
 CC viral or microbial cysteine protease (e.g. human coronavirus or
 CC gingipain), or protozoan cysteine protease (e.g. Trypanosoma,
 CC Schistosoma, Leishmania or Plasmodium protease). They can be used
 CC e.g. for inhibiting cancer cell growth, tumor progression or tumour
 CC metastasis, or microbial cell or viral growth (e.g. inhibiting
 CC hepatitis A virus 3C proteinase, hepatitis C virus endopeptidase 2,
 CC picornain 3C rhinovirus protease, foot and mouth disease virus 1,
 CC proteinase, encephalomyelitis virus endopeptidase 2, picornain 2A
 CC protease), treating allergic response symptoms (e.g. inhibiting
 CC protease Der p1); treating neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease, multiple sclerosis) and
 CC disorders resulting from ischaemic-reperfusion injury (e.g. stroke,
 CC myocardial infarction, transplantation, vascular injury or
 CC cardiovascular collapse or shock); treating inflammatory and
 CC degenerative diseases (e.g. rheumatoid arthritis, osteoarthritis or
 CC periodontal disease); or treating pulmonary diseases (e.g. asthma or
 CC emphysema). They can also be used for detecting or quantifying cysteine
 CC protease activity in a sample, mixture, biological fluid or tissue; for
 CC purifying cysteine protease in a sample; or as antibacterial agents,
 CC herbicides, fungicides or pesticides.
 XX
 SQ Sequence 4 AA;

Query Match 80.0%; Score 16; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
 |||
 Db 1 LEP 3

RESULT 4
 AAY15640
 ID AAY15640 standard; Peptide; 4 AA

XX
 AC AAY15640;
 XX 27-JUL-1999 (first entry)

DE Peptide used to make fluorescent reporter molecules

XX Fluorogenic; fluorescent reporter molecule; enzyme substrate;
 KW apoptosis; protease, peptidase; apoptosis cascade; cancer;
 KW chemotherapeutic agent; cell death; viral protease activity.

XX Synthetic.

OS WO9918956-A1.

PN 22-APR-1999.

PD 09-OCT-1998; 98WO-US21231.

PF 03-MAR-1998; 98US-0035661.

PR 10-OCT-1997; 97US-0081592

XX (CYTO-) CYTOWIA INC.
 PA Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
 XX WPI; 1999-312448/26.
 XX New fluorogenic or fluorescent reporter molecules
 PT Claim 6, Page 165, 203pp; English.
 XX AAY15618-Y15759 represent peptides used to make the fluorogenic or
 CC fluorescent reporter molecules of the invention. These molecules
 CC contain a peptide moiety (e.g. present sequence) which acts as a
 CC substrate for enzymes involved in apoptosis or protease or peptidase
 CC enzymes. The compounds can be used as fluorogenic or fluorescent
 CC substrates for enzymes. Depending on the peptide moiety used, the
 CC fluorescent molecules can be used for detecting or measuring the
 CC activity of an enzyme involved in the apoptosis cascade in cells; to
 CC determine whether a test compound has an effect on an enzyme involved
 CC in the apoptosis cascade in cells; for determining the sensitivity of
 CC an animal with cancer to treatment with chemotherapeutic agents or
 CC determining whether a test substance inhibits, prevents, causes or
 CC enhances cell death of test cells; for detecting or measuring the
 CC activity of a viral protease in cells; for determining whether a test
 CC compound has an effect on the activity of a viral protease in cells;
 CC and for measuring the activity or determining whether a test substance
 CC has an effect on the activity of a protease or peptidase in cells.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 20; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
 |||
 Db 1 LEP 3

RESULT 5
 AAB28671
 ID AAB28671 standard; peptide; 4 AA.

XX
 AC AAB28671;
 DT 13-FEB-2001 (first entry)

DE Chemotactic peptide pepL.

XX Chemotactic, osteopontin, vulnery, antiarthritis, antipsoriatic;
 KW cytostatic; antitumor; antiinflammatory; osteopathic;
 KW wound healing; cell migration; chemotaxis; atherosclerosis, cancer;
 KW angiotensin-associated disease; arthritis; psoriasis; haemangioma;
 KW ocular neovascularisation; cell apoptosis; nitrous oxide production;
 KW inflammation; osteoporosis; immune disease.

OS Mammalia.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

XX WO2000063247 A2.

XX 26-OCT-2000

XX 17-APR-2000; 2000WO-US10344.

XX 15-APR-1999; 99US-0129764.

XX (CHIL) CHILDRENS MEDICAL CENT.

XX PI Ashkar S;
 XX DP WPI: 2000-087150/57.
 XX
 XX New osteopontin derived chemotactic and inhibitory peptides, useful for
 PT promoting scarless wound healing, modulating cellular chemotaxis,
 PT treating formation of atherosclerotic plaques and preventing metastasis
 PT
 XX
 XX Claim 17; Page 43; 54pp; English.
 XX
 XX The present sequence is an osteopontin-derived chemotactic peptide.
 CC Such chemotactic peptides are useful for promoting scarless wound
 CC healing, modulating chemotaxis and promoting cell migration to a target
 CC site in a cell of a subject. They are also used for modulating cellular
 CC chemotaxis in a mammalian cell such as smooth muscle cell, a macrophage,
 CC an endothelial cell, a vascular cell and a tumorigenic cell. They are
 CC useful for treating the formation of atherosclerotic plaques in a
 CC subject. The peptides are used for preventing metastasis, treating an
 CC angiogenic-associated disease such as arthritis, psoriasis, haemangioma,
 CC tumour metastasis or ocular neovascularisation. They are also used for
 CC activating cell apoptosis, for modulating nitrous oxide production and
 CC for inducing chemotaxis. The peptides are useful for diagnosing, treating
 CC and preventing tumour metastasis, inflammation, osteoporosis and immune
 CC diseases. They can also be used to enhance an immune response by
 CC attracting macrophages.

XX Sequence 4 AA;

Query Match 75.0%; Score 14; DB 21; Length 4;
 Best Local Similarity 50.0%; Pred. No. 7 8e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPP 4
 DB 1 MLDP 4

RESULT 6

AAB22909

ID AAB22909 standard; peptide; 4 AA.

XX AAB22909;

DT 10-JAN-2001 (first entry)

XX Granzyme B substrate recognition sequence, SEQ ID NO:100.

XX Bioreceptor protein; fusion protein; recognition site;
 KW cellular targeting sequence; cellular localisation; fluorescent protein;
 KW protease activity detection; toxin detection; cellular stress detection;
 KW drug discovery; cell based screening; protease recognition site;
 KW cleavage site.

XX Unidentified

XX WQ2000050872-A2

XX 31-AUG-2000

XX 25 FEB 2000, 2000WO USC4794.

XX 26-FEB-1999; 99US 0122152.

XX 08-MAR-1999; 99US-0123399.

XX 12-JUL-1999; 99US 0352171

XX (CELL-1) CELLULINICS INC.

XX Giuliano KA, Kapur R;

XX WPI: 2000-594086/56.

XX N-ESDB; AAB22909

XX Automated cell-based characterization of toxin by contacting cells
 PT containing luminescent reporter molecules with test substance and
 PT analyzing optically -
 XX
 XX Example 11, Fig 20B; 336pp; English.
 XX
 XX The invention relates to systems, methods and reagents for cell-based
 CC screening or detection of compounds which affect particular biological
 CC functions. The methods of the invention utilise fluorescent bioreceptor
 CC molecules which, when acted on by a compound of interest, cause an
 CC alteration in the cellular distribution of at least the fluorescent
 CC moiety. In one embodiment, the biosensors comprise heat shock proteins
 CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
 CC protein (GFP), or derivatives thereof). Such biosensors are located in
 CC the cytoplasm, but on stress activation translocate to the nucleus. In
 CC another embodiment bioreceptor proteins can be used to detect protease
 CC activity. Such protease bioreceptor fusion proteins comprise one or more
 CC fluorescent proteins; a recognition signal which is cleaved by the
 CC protease; and at least one cellular localisation signal. The latter two
 CC components may be components of a single protein which is acted upon by
 CC the protease, or may be from heterologous sources. Due to the
 CC localisation signal, the bioreceptor protein is localised to a
 CC particular region of the cell. Once acted on by the protease of interest,
 CC the fluorescent protein is cleaved from the localisation sequence, and
 CC is free to migrate to other locations within the cell. The presence of a
 CC second localisation signal attached to the fluorescent protein enables
 CC the fluorescent protein to be directed to a different cellular
 CC compartment after cleavage of the protease recognition sequence. The
 CC change in distribution of the fluorescent protein can be detected using
 CC imaging methods with a high degree of spatial resolution. The methods
 CC and biosensors of the invention can be used to investigate a wide range
 CC of cellular activities and to screen compounds which modulate these
 CC activities. Biosensors containing a recognition site for caspase, for
 CC example, may be used for the screening of compounds which modulate
 CC apoptosis, while biosensors containing other protease recognition sites
 CC may be used for the detection of proteolytic toxins (such as anthrax
 CC lethal factor). The method provides improved target validation and
 CC candidate compound optimisation by combining many cell screening formats
 CC with fluorescence-based molecular reagents and computer-based feature
 CC extraction, data analysis and automation, resulting in increased
 CC quantity and speed of data collection and faster evaluation of drug
 CC candidates. Sequences AAB22886-B22920 and AAB22935 represent protease
 CC recognition sites which may be used as components of biosensor fusion
 CC proteins of the invention.

Sequence 4 AA;

Query Match 70.0%; Score 14; DB 21; Length 4;

Best Local Similarity 66.7%; Pred. No. 7 8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 1 IEP 3

RESULT 7

AAY79611

ID AAY79611 standard; peptide; 4 AA

XX AAY79611;

XX 20-AUG-2000 (first entry)

XX Granzyme-B substrate recognition sequence.

XX Increase; biosensor; granzyme-B; substrate recognition sequence;
 KW cell screening; assay; analysis; drug discovery.

XX Unidentified.

XX WQ200006408 A2

XX 11-MAY-2000
 XX 29-OCT-1999; 99WO-US26431
 XX 30-OCT-1998; 98US-0106308
 XX 26-MAY-1999; 98US-0136078
 XX (CELL-) CELLCOMICS INC.
 XX Giuliano KA, Bright G, Olson K, Burroughs Tencza S;
 XX WPI, 2000-365644/31.
 XX N PQR; AAA27600.
 XX Recombinant nucleic acid encoding a protease biosensor useful for
 PT fluorescence based cell and molecular biochemical assays for drug
 PT discovery comprising three operably linked nucleic acid sequences
 XX
 PS Claim 15; Fig 209; 218pp; English.
 XX
 CC The present sequence is that of a granzyme-B substrate
 CC recognition sequence, which can be included in novel recombinant
 CC protease biosensors (see of the invention). The PRs (see AA79623-64)
 CC comprise a first domain (see AA79659-87) comprising at least 1
 CC detectable polypeptide signal, a second domain (see AA79689-92)
 CC comprising at least 1 protease recognition site, such as the
 CC present sequence; and a third domain (see AA79693-97) comprising at
 CC least 1 reactant target sequence. A recombinant nucleic acid (see
 CC AA79627-41) encoding the PR, an expression vector, and a genetically
 CC engineered host cell are also claimed. A claimed method for
 CC identifying compounds that modify protease activity in a cell
 CC involves contacting a host cell that possesses the recombinant PR
 CC with a test compound, and determining the PR distribution in the
 CC host cell, where changes in the distribution of the PR are
 CC correlated with modification of protease activity by the test
 CC compound. Claimed kits for identifying compounds that modify
 CC protease activity in a host cell include the recombinant nucleic
 CC acid, or the recombinant PR, or the vector, or the host cell. The
 CC PR is useful in high content screens to detect in vivo activation
 CC of enzymatic activity, and to identify specific activity based on
 CC cleavage of a known recognition motif.
 XX
 SQ Sequence 4 AA;
 Query Match 70.0%; Score 14; DB 21; Length 4;
 Best Local Similarity 66.7%; Pred No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEP 4
 Db 1 IEP 3
 RESULT 8
 AA79804
 ID AA79804 standard; peptide; 4 AA.
 XX
 AC AA79804;
 XX
 DT 22-MAY-2000 (first entry)
 XX
 DE Fluorophore-labelled granzyme B substrate peptide, SEQ ID NO. 23.
 XX
 KW protease substrate; fluorescent label; fluorophore; rhodamine.
 KW blocking group; halobenzoyl group; cleavage; caspase; viral protease;
 KW methionine aminopeptidase type 2; MetAP 2; drug screening.
 XX
 OS Synthetic.
 XX
 PN WQ200004914-A1.
 XX
 PD 03-FEB-2000.

XX 21-JUL-1999; 99WO-US16423.
 XX 31-JUN-1998; 98US-089742.
 XX (CYTO-) CYTOVIA INC.
 XX (ZHAN/) ZHANG H.
 XX (CAIS/) CAI S X.
 XX (DREW/) DREW J A.
 XX (YANG/) YANG W.
 XX Zhang H, Cai SX, Drewe JA, Yang W;
 XX WPI, 2000-195079/17.
 XX New fluorescently labeled amino acids or peptides, used in substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group.
 XX
 PS Claim 3; Page 100; 174pp; English.
 XX
 CC The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-F, where Y represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC fluorophore), and the peptide Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detection intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus 1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP 2). The peptides are particularly useful to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured with recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP 2 are
 CC potential anti-angiogenic or anticancer agents. Sequences
 CC AA79627-41 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.
 XX
 SQ Sequence 4 AA;
 Query Match 70.0%; Score 14; DB 21; Length 4;
 Best Local Similarity 66.7%; Pred No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEP 4
 Db 1 IEP 3
 RESULT 9
 AAU79766
 ID AAU79766 standard; peptide; 4 AA.
 XX
 AC AAU79766;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE Chicken bone derived peptide #1, useful as ACE inhibitor.
 XX
 KW Angiotensin converting enzyme inhibitor; ACEI; health food;
 KW food additive; pharmaceutical product; lowering blood pressure;
 KW hypertension; chicken essence by-product; chicken bone.
 XX
 OS Gallus sp.
 XX
 PN JP2001163496-A
 XX
 PD 19-JUN-2001.
 XX
 PF 03-APR-2000; 2000JP-0105410.

fluorescence produced. This is particularly useful for detecting enzymes such as proteases and caspases, which may be linked to cancer metastasis. The present sequence is a caspase inhibitor substrate used in the exemplification of the invention

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SQ      Sequence      4 AA;
Query Match      70.0%; Score 14; DB 22; Length 4;
Best Local Similarity 66.7%; Pred. NO. 7.8e05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 LEP 4
      .!!
Db      1 LEP 3

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RESULT 12	
AAAR29759	
ID	AAAR29759 standard; peptide: 4 AA.
XX	
XX	AAAR29759;
XX	
DT	28 FEB-2001 (first entry)
XX	
XX	Escherichia coli ribosomal protein L16 N-terminus.
DE	
XX	
PF	Recombinant human haemoglobin, rHb1, bacterial expression,
KW	N-terminal methionine methylation signal; demethylation,
XX	Escherichia coli; non-immunogenic; pharmaceutical composition.
XX	
OS	Escherichia coli.
XX	
PN	US6140071-A.
XX	
PD	31-OCT-2000.
XX	
PF	27 JAN-1994; 94US-0188374.
XX	
PR	27 JAN 1994, 94US-0188374.
XX	
PA	(SOMA-1) SOMATOGEN INC.
XX	
PI	Aiken JF, Apostol IZ, Levine JD, Lippincott JA;
XX	
DR	WPI: 2001-048957/06

Disclosure: Column 1; 26pp; English.

The invention relates to a method of decreasing the amount of N-terminal methionine methylation on a protein expressed in a bacterium. The bacterial methyltransferase which directs N-terminal methionine methylation recognises proteins which have a proline residue at position 4 (e.g., the bacterial ribosomal protein L16 and the bacterial chemotaxis protein CheZ). The method comprises introducing mutations into the DNA encoding the protein so that residue 4 is a non-proline residue, thereby reducing the degree of N-terminal methylation when the protein is expressed in a bacterium. The method is useful for decreasing methylation of a protein, particularly a recombinantly produced protein. The demethylated protein can be used in a pharmaceutical composition for the treatment of a disease but with less likelihood of eliciting an immunological response. These demethylated proteins may be used as therapeutic agent for the treatment and/or amelioration of disease or symptoms associated with a disease. The exemplifications describe the expression of a recombinant human haemoglobin construct (Hb1.1) in *Escherichia coli*, and its modification such that residue 4 of the α -chain of the recombinant haemoglobin is altered from proline to a non-proline residue. The present sequence represents a peptide referred to in the disclosure of the invention.

[illegible]

XX	RESULT 13
XX	AAE19128
XX	ID AAE19128 standard; peptide; 4 AA.
XX	AAE19128;
XX	AC
XX	2: MAY 2002 (first entry)
XX	DE Granzyme B peptide.
XX	KL luciferase; enzyme; protease; cell growth, apoptosis; therapeutic
XX	KW cell death; granzyme B.
XX	OS Unidentified.
XX	PN WO200206458-A2.
XX	PD 24 JAN. 2002.
XX	PF 17-JUL-2001; 2001WO-US22478.
XX	PP 19-JUL-2000; 2000US-0619047.
XX	PP (CHEM-) CHEMICON INT INC.
XX	PI Leng J;
XX	PI
XX	PP 1; 2002-195809/25.
XX	PP New purified luciferase polypeptide, useful for identifying protease-
XX	PP activity modulators, comprises recognition site cleavable by protease,
XX	PP where cleavage of polypeptide results in decreased luciferase activity
XX	PP
XX	PP Claim 63; Page 25; 56pp; English.
XX	PP

Claim 63: Page 25; 56pp; English.

The invention relates to a purified polypeptide having luciferase activity and a recognition site specifically cleavable by a protease, where cleavage results in a decrease in luciferase activity. The polypeptide comprises a localisation sequence which is linked to the luciferase polypeptide by the cleavable recognition sequence. The polypeptide is useful for identifying a protease (apoptosis) activity modulator, an inhibitor of apoptosis and for detecting luciferase activity in a sample. The polypeptide is used for characterising and identifying cellular processes associated with metabolism, cell growth and cell death e.g. apoptosis and for measuring protease activity. The protease measurement methods are useful for characterising, identifying cellular biochemical pathways as well as identifying diagnostic and agents for modulating diseases or disorders associated with biochemical pathways. The polypeptide is also useful as a substrate to study agents or conditions that cleave the recognition site and for determining amount of protease in a sample and for monitoring the activity of protease inside a cell that expresses a recombinant luciferase. The present sequence is granzyme B peptide used in the invention.

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AA
SQ Sequence 4 AA;
Query Match 70.0%; Score 14; DB 23; Length 4;
Blast Local Similarity 66.7%; Pred No 7.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 2 LEP 4
DB 1 IEP 3

RESULT 14
AAM50406
ID AAM50406 standard; Peptide; 4 AA.
XX
AC AAM50407;
XX
DT 12-MAR-2002 (first entry)
XX
DE Tumour associated activatable guarding moiety.
XX
KW Magnetic resonance imaging; MRI; cancer; detection;
KW contrasting agent; tumour associated activatable guarding moiety;
KW TAAGM.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 4 /note= "N-terminal acetyl"
FT Modified-site 4 /note= "C-terminal pNA"
XX
PN WO200182976-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US14470
XX
PR 04-MAY-2000; 2000US-201816P.
XX
PP 17-NOV-2000; 2000US-0715859.
XX
PA (RESE ) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Meade TJ;
XX
WPI; 2002-075134/10.
XX
PT New magnetic resonance imaging contrast agents for detection of
PT cancerous cells and tissues -
XX
PS Disclosure; Page 27; 61pp; English.
XX
CC The present peptide is an example of a tumour associated activatable
CC guarding moiety (TAAGM) that is used in a preferred embodiment of
CC the invention. A claimed magnetic resonance imaging (MRI) contrast
CC agent composition comprises: a gadolinium (III) ion bound to a first
CC chelator such that the ion has coordination atoms in at least 7 of
CC its coordination sites; and a TAAGM covalently attached to the first
CC chelator which hinders the rapid exchange of water in the remaining
CC coordination sites of the Gd(III) ion. The novel MRI contrast
CC agents can target substances that are associated with cancer. By
CC using a targeting moiety, the MRI agents become more effective,
CC discriminatory and selective with regard to signal detection of
CC disease pathology.
XX
SQ Sequence 4 AA;
Query Match 70.0%; Score 14; DB 23; Length 4;
Best Local Similarity 66.7%; Pred. No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
DB 1 IEP 3

RESULT 16
AAM50466
ID AAM50466 standard; Peptide; 4 AA.
XX
AC AAM50466;
XX
DT 12-MAR-2002 (first entry)
XX

```

DE Tumour associated activatable guarding moiety.
 XX
 XX Magnetic resonance imaging; MRI; cancer; detection;
 KW contrasting agent; tumour associated activatable guarding moiety;
 KW TAAGM.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1
 FT Modified-site 4 /note= "N-terminal acetyl"

FT Modified-site 4 /note= "C-terminal aldehyde (pseudo acid)"

XX WO200182976 A2

XX 08 NOV 2001

XX 04 MAY 2001; 2001WO-US14470.

XX 04 MAY 2000; 2000US-201816P

XX 17 NOV 2000; 2000US-0715859.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Meade TJ;

XX WPI; 2002-075134/10.

XX New magnetic resonance imaging contrast agents for detection of
 PT cancerous cells and tissues

XX Disclosure; Page 29; 61pp; English.

XX The present peptide is an example of a tumour associated activatable
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast
 CC agent composition comprises: a gadolinium (III) ion bound to a first
 CC chelator such that the ion has coordination atoms in at least 7 of
 CC its coordination sites; and a TAAGM covalently attached to the first
 CC chelator which hinders the rapid exchange of water in the remaining
 CC coordination sites of the Gd(III) ion. The novel MRI contrast
 CC agents can target substances that are associated with cancer. By
 CC using a targeting moiety, the MRI agents become more effective,
 CC discriminatory and selective with regard to signal detection of
 CC disease pathology.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 23; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 1 IEP 3

RESULT 17

AAM50470

ID AAM50470 standard; Peptide; 4 AA.

XX AAM50470;

XX 12-MAR-2002 (first entry)

XX Tumour associated activatable guarding moiety.

XX Magnetic resonance imaging; MRI; cancer; detection;
 KW contrasting agent; tumour associated activatable guarding moiety;
 KW TAAGM.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 4 /note= "C-terminal aminomethyl coumarin"

XX WO200182976 A2.

XX 08 NOV 2001.

XX 04 MAY 2001; 2001WO-US14470

XX 04 MAY 2000; 2000US-201816P.

XX 17 NOV 2000; 2000US-0715859.

XX (RESE) RESEARCH CORP TECHNOLOGIES INC.

XX Meade TJ;

XX WPI; 2002-075134/10.

XX New magnetic resonance imaging contrast agents for detection of
 PT cancerous cells and tissues

XX Disclosure; Page 28; 61pp; English.

XX The present peptide is an example of a tumour associated activatable
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast
 CC agent composition comprises: a gadolinium (III) ion bound to a first
 CC chelator such that the ion has coordination atoms in at least 7 of
 CC its coordination sites; and a TAAGM covalently attached to the first
 CC chelator which hinders the rapid exchange of water in the remaining
 CC coordination sites of the Gd(III) ion. The novel MRI contrast
 CC agents can target substances that are associated with cancer. By
 CC using a targeting moiety, the MRI agents become more effective,
 CC discriminatory and selective with regard to signal detection of
 CC disease pathology.

XX Sequence 4 AA;

Query Match 70.0%; Score 14; DB 23; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 1 IEP 3

RESULT 18

AAM50471

ID AAM50471 standard; Peptide; 4 AA.

XX AAM50471;

XX 12-MAR-2002 (first entry)

XX Tumour associated activatable guarding moiety.

XX Magnetic resonance imaging; MRI; cancer; detection;
 KW contrasting agent; tumour associated activatable guarding moiety;
 KW TAAGM.

XX Synthetic.

XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 4 /note= "C-terminal pNA"

PN WC200182976-A2.
 XX 08-NOV-2001.
 XX 04-MAY-2001, 2001W-0514400
 XX 04-MAY-2000, 2000US-201816P
 PF 17-NOV-2000, 2000US-0715859.
 XX (PSE) RESEARCH CORP TECHNOLOGIES INC.
 PA Meade TJ;
 XX WPI; 2002-075114/10.
 XX New magnetic resonance imaging contrast agents for detection of
 PT cancerous cells and tissues -
 XX Disclosure; Page 28; 6lpp; English.
 XX The present peptide is an example of a tumour associated activatable
 CC guarding moiety (TAAGM) that is used in a preferred embodiment of
 CC the invention. A claimed magnetic resonance imaging (MRI) contrast
 CC agent composition comprises: a gadolinium (III) ion bound to a first
 CC chelator such that the ion has coordination atoms in at least 7 of
 CC its coordination sites, and a TAAGM covalently attached to the first
 CC chelator which hinders the rapid exchange of water in the remaining
 CC coordination sites of the Gd(III) ion. The novel MRI contrast
 CC agents can target substances that are associated with cancer. By
 CC using a targeting moiety, the MRI agents become more effective,
 CC discriminatory and selective with regard to signal detection of
 CC disease pathology.
 XX Sequence 4 AA;
 SQ
 Query Match 70.0%; Score 14; DB 23; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 2, Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEP 4
 DB 1 IEP 3
 RESULT 19
 AAP71434
 XX AAP71434 standard; Protein; 4 AA.
 AC AAP71434;
 DT 03-MAY-1991 (first entry)
 XX Immunomodulator peptide #10 inhibits HIV-T4 interaction.
 DE AIDS; T4 cell receptor; immunomodulation.
 XX Synthetic.
 OS WO8703601-A.
 PN 18-JUN-1987.
 PD 08-DEC-1986; 86WO-4002717.
 XX 01-DEC-1985, 85FR-0018155.
 XX (INSP) INST PASTEUR.
 PA (AUPR/) AUPRAY C.
 XX Auffray C, Montagnier L, Klatzmann D, Charron D;
 XX WPI; 1987-177935/25.
 DR
 XX

PT New peptide derivs. contg. specified exposed tetra-peptide
 PT sequences - inhibiting interaction of AIDS virus with T4 cell
 PT receptors
 XX Claim 18; Page 50; 57pp; French.
 XX The tetrapeptide corresponds to the conserved sequence immediately
 CC preceding the RPS peptide motif of the Type II HLA antigens of
 CC H1V1II, ARV2, LAV1a and IV. It is used to provoke production of
 CC monoclonal antibodies specific to the peptide.
 CC See also AAP71422-P71433 and AAP71435-7.
 XX Sequence 4 AA;
 SQ
 Query Match 65.0%; Score 13; DB 8; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3, Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLE 3
 DB 1 VLE 3
 RESULT 20
 AAP23726
 ID AAP23726 standard; peptide, 4 AA.
 XX AAP23726,
 AC AAP23726,
 DT 26-OCT-1992 (first entry)
 XX ACE inhibitor peptide.
 DE ACE inhibitor peptide.
 XX Angiotensin converting enzyme; vasodepression.
 XX Synthetic.
 OS JP04091097-A
 PN 24-MAR-1992.
 PD 03-AUG-1990; 90JP-0205000.
 PF 03-AUG-1990; 90JP-0205000.
 XX (NISS) NISSHIN FLOUR MILL KK.
 PA WPI; 1992-148004/18.
 DR New peptide as ACE inhibitor - with vasodepressive and
 PT vasopressive inhibiting activity
 XX Claim 1; Page 1; 7pp; Japanese.
 XX By admin. of a very small amt. of the ACE inhibitor, vasodepressor
 CC activity and vasopressor inhibiting activity can be obtd. Also, as it
 CC is a white water soluble powder, it can be administered directly or as
 CC an aq. soln, orally or parenterally. It can be prepd. easily by
 CC simple chemical synthesis.
 XX Sequence 4 AA;
 SQ
 Query Match 65.0%; Score 13; DB 13; Length 4;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 2, Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 LEP 4
 DB 1 LQP 3
 RESULT 21
 AA093983

ID AAW93983 standard; peptide; 4 AA.
 AC AAW93983;
 XX
 DT 01-JUL-1999 (first entry)
 XX
 DE Antineoplastic peptide 4.
 XX
 KW Tetrapeptide; tumour; delactarin; antineoplastic activity; lung, breast,
 PW intestine; bladder; rectum; uterus; prostate; leukaemia; lymphoma,
 KW neoplastic disease.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "Me2-Val"
 FT Modified-site 3 /note= "Me-Val"
 FT Modified-site 4 /note= "Pro-OMe"
 FT
 FT DE4415998-A1.
 PN
 XX
 PD 09 NOV-1995.
 XX
 PF 06 MAY-1994; 94DE-4415998.
 XX
 PR 06 MAY-1994; 94DE-4415998.
 XX
 PA (BADI) BASF AG.
 XX
 PI Amberg W, Bernard H, Buschmann E, De Perzelli P;
 PI Haupt A, Janitschke L, Janssen B, Karl U, Kling A;
 PI Mueller S, Ritter K, Thyges M, Zierke T;
 XX
 DR WPI; 1995-393582/51.
 XX
 XX Prepn. of proline contg. tetra-peptide derivs. - comprises
 FT condensing tri-peptide with protected amino acid, deprotection, and
 PT N-di-methylation, useful as e.g. intermediates for dolastatin
 XX
 PS Example 4; Page 6; 8pp; German.
 XX
 CC This invention describes a method for the production of tetrapeptides
 CC which comprises reacting a tripeptide with an amino acid, removing Z and
 CC methylating the free amino group twice. R1, R4 = 1-6C alkyl, and Z =
 CC optional ring substituted benzyloxycarbonyl. The products of the
 CC invention are intermediates for dolastatin 15 which have high
 CC antineoplastic activity. The peptides of the invention are active against
 CC solid tumours (of lung, breast, intestine, bladder, rectum, uterus and
 CC prostate), leukaemia, lymphoma and other neoplastic diseases. The
 CC peptides can now be produced from material available in large quantities,
 CC without racemisation and without requiring very expensive or hazardous
 CC reagents.
 XX
 SQ Sequence 4 AA;
 Query Match 65.0%; Score 13; PR 16; Length 4;
 Best Local Similarity 75.0%; Pred. No. 7 Re+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 VLEP 4
 DB 1 VLVP 4
 RESULT 22
 AAW62052
 ID AAW62052 standard; peptide; 4 AA.
 AC AAW62052;
 XX

DT 11-SEP-1998 (first entry)
 XX
 DE Human erythropoietin peptide fragment T13.
 XX
 KW Human, erythropoietin, EPO, bone marrow, reticulocyte; red blood cell;
 PW expression; CHO, Chinese hamster ovary cell, diagnosis, blood disorder.
 XX
 OS Homo sapiens.
 XX
 PN AU688723-B.
 XX
 PD 19-FEB-1998.
 XX
 PF 02-DEC-1997; 97AU-0046867.
 XX
 PR 02-DEC-1997; 97AU-0046867.
 XX
 PA (KIP1) KIPIN AMGEN INC.
 XX
 PI Lin F;
 XX
 DR WPI; 1998-261957/24.
 XX
 XX Recombinant human erythropoietin - potentially useful for diagnosis
 PT and treatment of blood disorders
 XX
 PS Example 1, Page 25; 100pp; English.
 XX
 CC The present sequence represents a peptide fragment of human
 CC erythropoietin (EPO). The present invention describes recombinant
 CC human EPO which causes bone marrow cells to increase production
 CC of reticulocytes or red blood cells, where the polypeptide is the
 CC product of expression in CHO (Chinese hamster ovary) cells of an
 CC exogenous DNA sequence encoding human EPO. EPO is potentially
 CC useful in the diagnosis and treatment of blood disorders
 CC characterised by low or defective red blood cell production.
 XX
 SQ Sequence 4 AA;
 Query Match 65.0%; Score 13; DB 19; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 VLE 3
 DB 1 VLE 3
 RESULT 23
 AAY15644
 ID AAY15644 standard; Peptide; 4 AA.
 XX
 AC AAY15644;
 XX
 DT 27-JUL-1999 (first entry)
 XX
 DE Peptide used to make fluorescent reporter molecules.
 XX
 KW Fluorogenic; fluorescent reporter molecule; enzyme substrate;
 PW apoptosis; protease; peptidase; apoptosis cascade; cancer;
 PW chemotherapeutic agent; cell death; viral fitness activity.
 XX
 OS Synthetic.
 XX
 PN WO9918856-A1.
 XX
 PD 22-APR-1999.
 XX
 PF 09-OCT-1998; 98WO US21231.
 XX
 PR 03-MAR-1998; 98US-0033661.
 PF 10-OCT-1997; 97US-0061582.
 XX

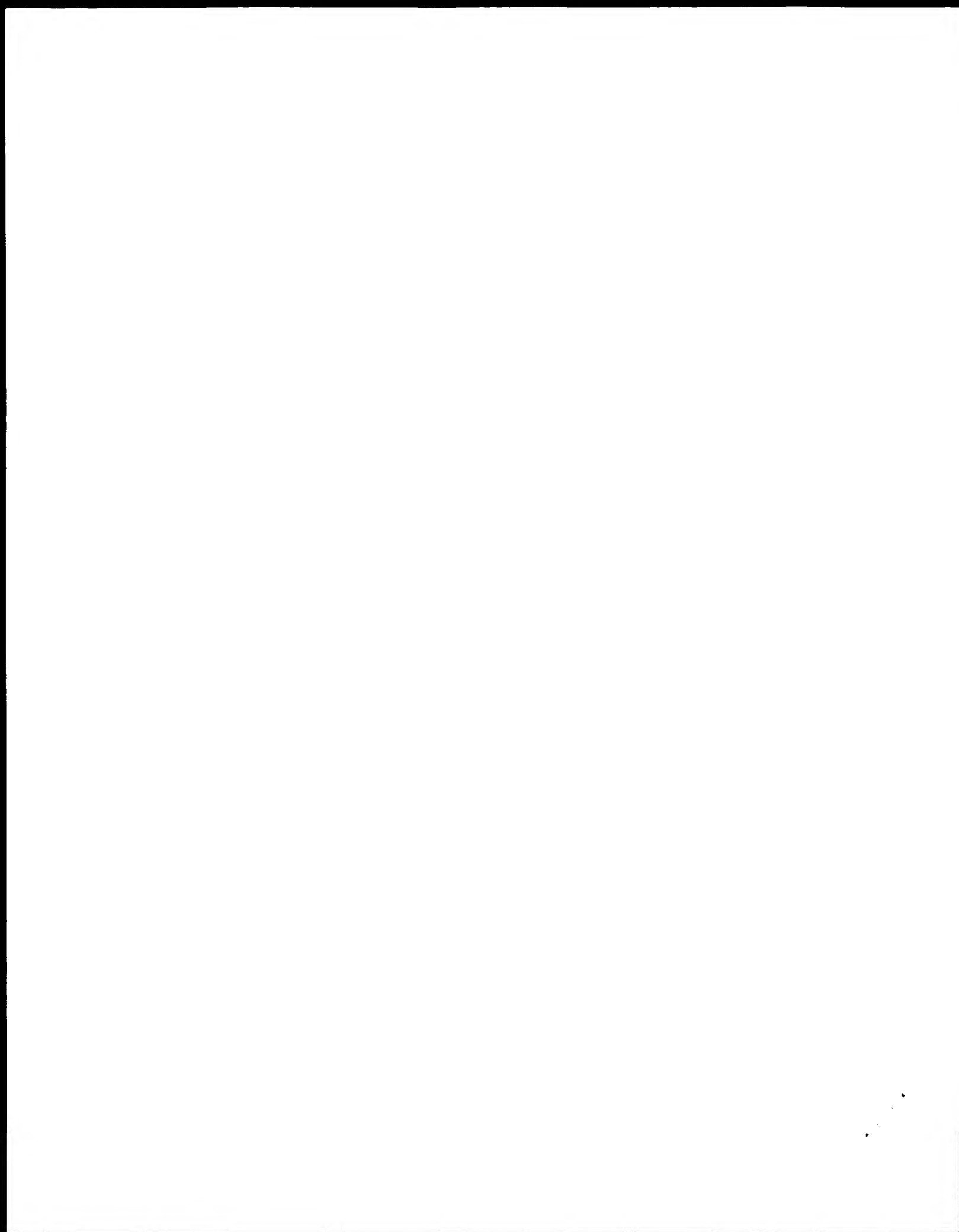
PA (CYTO-) CYTOVIA INC.
XX Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
XX WPI; 1999-312448/26.
XX New fluorogenic or fluorescent reporter molecules
PT Claim 6, Page 167, 202pp; English.
XX AAY15618-Y15759 represent peptides used to make the fluorogenic or
XX fluorescent reporter molecules of the invention. These molecules
XX contain a peptide moiety (e.g. present sequence) which acts as a
XX substrate for enzymes involved in apoptosis or protease or peptidase
XX enzymes. The compounds can be used as fluorogenic or fluorescent
XX substrates for enzymes. Depending on the peptide moiety used, the
XX fluorescent molecules can be used for detecting or measuring the
XX activity of an enzyme involved in the apoptosis cascade in cells; to
XX determine whether a test compound has an effect on an enzyme involved
XX in the apoptosis cascade in cells; for determining the sensitivity of
XX an animal with cancer to treatment with chemotherapeutic agents or
XX enhancing cell death of test cells; for detecting or measuring the
XX activity of a viral protease in cells; for determining whether a test
XX compound has an effect on the activity of a viral protease in cells,
XX and for measuring the activity or determining whether a test substance
XX has an effect on the activity of a protease or peptidase in cells.
XX Sequence 4 AA;
SQ Query Match: 65.0%; Score 13, DB 20, Length 4;
Best Local Similarity 66.7%; Pred No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LEP 4
Db 1 VEP 3
RESULT 24
AAW83445
ID AAW83445 standard; peptide; 4 AA.
XX AAW83445;
XX 08-MAR-1999 (first entry)
XX Human growth hormone mutant peptide #5.
XX Human; growth hormone; hGH; phagemid particle; enzyme substrate;
XX fusion gene; phage protein coat.
XX Homo sapiens.
XX Synthetic.
XX US5846765-A.
XX 08-DEC-1998.
XX 16-MAY-1995; 95US-0441871.
XX 02-DEC-1993; 93US-0161692.
XX 03-DEC-1990; 90US-0621667.
XX 10-APR-1991; 91US-0683400.
XX 14-JUN-1991; 91US-0715300.
XX 09-AUG-1991; 91US-0743614.
XX 03-DEC-1991; 91WO-US09133.
XX 06-APR-1992; 92US-0864452.
XX 30-APR-1993; 93US-0050058.
XX 05-APR-1995; 95US-0418928.
XX 16-MAY-1995; 95US-0441871.
XX (GETH) GENENTECH INC.
XX PI Cai SX, Drewe JA, Keana JFW, Weber E, Zhang H;
XX WPI; 1999-059058/05.
XX Selection of polypeptide substrates - using phagemid particles
PT displaying polypeptide(s) as coat protein fusions
XX Example 8; Column 32; 81pp; English.
XX The present invention describes a method for selecting novel polypeptide
XX substrates. The method comprises: (a) constructing a replicable
XX expression vector comprising a transcription regulatory element operably
XX linked to a gene fusion; (b) mutating the vector at one or more selected
XX positions within the second gene thereby forming a family of related
XX plasmids encoding substrate peptides; (c) transforming suitable host
XX cells with the plasmids; (d) infecting the transformed host cells with a
XX helper phage having a gene encoding the phage coat protein, the phage
XX the transformed infected host cells under conditions suitable for forming
XX recombinant phagemid particles containing at least a portion of the
XX plasmid and capable of transforming the host, the conditions being
XX adjusted so that no more than a minor amount of phagemid particles
XX display more than one copy of the fusion protein on the surface of the
XX particle, (f) exposing the phagemid particles to a process capable of
XX modifying at least one covalent bond of an amino acid in the substrate
XX peptide of at least a portion of the phagemid particles; (g) contacting
XX the family of exposed phagemid particles with an affinity molecule, where
XX the affinity molecule has affinity for the amino acid residue having the
XX modified covalent bond; and (h) separating the phagemid particles that
XX bind to the affinity molecule from those that do not bind. The selection
XX method is used for identifying enzyme substrates. The present sequence
XX represents a human growth hormone mutant peptide from an example of the
XX present invention.
XX Sequence 4 AA;
SQ Query Match: 65.0%; Score 13; DB 20; Length 4;
Best Local Similarity 66.7%; Pred No. 7.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 2 LEP 4
Db 2 LDP 4
RESULT 25
AAY80808
ID AAY80808 standard; peptide; 4 AA.
XX AAY80808;
XX 22 MAY-2000 (first entry)
XX Fluorophore-labelled granzyme B substrate peptide, SEQ ID NO:27.
XX Protease substrate; fluorescent label; fluorophore; rhodamine;
XX blocking group; halogenoaryl group; cleavage; catpase; viral protease;
XX methionine aminopeptidase type 2; MetAP 2; drug screening.
XX Synthetic.
XX WO200004914-A1
XX 03-FEB-2000.
XX 21-JUL-1999; 99WO-US16423.
XX 21-JUL-1999; 99US-0094642.
XX (CYTO-) CYTOVIA INC.
XX (ZHAN/) ZHANG H.
XX (CAIS/) CAI S X.
XX (DREW/) DREWE J A.

PA (YANG/) YANG W.
 XX Zhang H, Cai SX, Drewe JA, Yang W;
 XX WPI: 2000-195079/17
 XX New fluorescently labeled amino acids or peptides, used as substrates
 PT for detecting enzymes or their modulators, e.g. anticancer or antiviral
 PT agents, contains a halobenzoyl N-blocking group
 XX
 PS Claim 3; Page 100; 174pp; English.
 XX
 CC The invention relates to fluorescently labelled peptides containing
 CC a halobenzoyl group on the fluorophore. They are of the structure
 CC peptide-Y-Z, where Z represents a halo-substituted benzoyl blocking
 CC group, Y is a fluorescent or fluorogenic moiety (preferably a
 CC rhodamine), and the peptide-Y bond is cleavable by the enzyme being
 CC assayed. The labelled peptides are reporters for detecting intracellular
 CC proteolytic enzymes, particularly caspases and other enzymes involved in
 CC apoptosis; viral proteases (e.g., HIV, herpes simplex virus-1, human
 CC cytomegalovirus and hepatitis C virus proteases); and methionine
 CC aminopeptidase type 2 (MetAP-2). The peptides are particularly used to
 CC identify modulators of these enzymes which may be potentially useful as
 CC agents for treating conditions such as cancer, neurodegeneration,
 CC autoimmune diseases, myocardial infarction and viral infection.
 CC Modulators identified may also be used to prolong the life of cells being
 CC cultured for recombinant protein production, or to monitor the treatment
 CC of cancer with chemotherapeutic agents. Inhibitors of MetAP-2 are
 CC potential anti-angiogenic or anticancer agents. Sequences
 CC AAYAN742 YAN016 represent peptides, some of which are specifically
 CC claimed, which may be used in assay methods according to the invention.
 XX
 SQ Sequence 4 AA;

Query Match 65.0%; Score 13; DB 21; Length 4;
 Best local Similarity 66.7%; Pred.No. 7.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEP 4
 DB 1 VEP 3

Search completed: March 5, 2003, 08:38:32
 Job time : 34 secs



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OM protein - protein search, using sw model

Run 3: Mar 5, 2003, 09:43:33, Search time 34.34 mins
(without alignment)
4.961 Million cell updates/sec

Title: US-09-732-411-15

Perfect score: 20
Sequence: 1 VLEP 4

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Gapop 10.0, Gapext 0.5

Searched: 18454 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 1965

Minimum DB seq length: 0
Maximum DB seq length: 4

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database: Published Applications AA*
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13: /cgn2_6/prodata/1/pubaa/US06_NEW_PUB_PEP*
14: /cgn2_6/prodata/1/pubaa/US06_PUBCOMB_PEP*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

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1	20	100.0	4	US-09-729-873-16
2	20	100.0	4	US-09-732-411-15
3	14	70.0	4	US-09-729-873-24
4	14	70.0	4	US-09-947-387-23
5	13	65.0	4	US-09-947-387-27
6	12	60.0	4	US-10-087-905-8
7	12	60.0	4	US-09-947-387-13
8	11	55.0	4	US-09-947-387-16
9	10	50.0	4	US-09-031-629A-1
10	10	50.0	4	US-09-494-409-26
11	10	50.0	4	US-09-742-096-26
12	10	50.0	4	US-10-029-191-16
13	10	50.0	4	US-10-115-704-9
14	10	50.0	4	US-10-207-951-8
15	10	50.0	4	US-10-207-951-9
16	10	50.0	4	US-09-729-873-21
17	10	50.0	4	US-09-804-017-4
18	10	50.0	4	US-09-934-765-742
19	10	50.0	4	US-09-804-733A-3

20	9	45.0	3	US-09-932-762A-10	Sequence 15, Appl
21	9	45.0	4	US-08-484-409-13	Sequence 13, Appl
22	9	45.0	4	US-09-947-387-24	Sequence 5, Appl
23	9	45.0	4	US-09-947-387-27	Sequence 7, Appl
24	9	45.0	4	US-10-045-801A-1	Sequence 1, Appl
25	9	45.0	4	US-10-101-447-101	Sequence 101, Appl
26	9	45.0	4	US-10-115-704-11	Sequence 11, Appl
27	9	45.0	4	US-10-115-704-12	Sequence 12, Appl
28	9	45.0	4	US-09-934-765-734	Sequence 17, Appl
29	9	45.0	4	US-09-802-077-60	Sequence 6, Appl
30	9	45.0	4	US-09-802-096-60	Sequence 60, Appl
31	9	45.0	4	US-09-244-694-167	Sequence 167, Appl
32	9	45.0	4	US-09-771-192-7	Sequence 7, Appl
33	9	45.0	4	US-09-834-765-729	Sequence 729, Appl
34	9	45.0	4	US-09-834-765-734	Sequence 734, Appl
35	9	45.0	4	US-09-834-765-734	Sequence 12, Appl
36	9	45.0	4	US-09-782-980-184	Sequence 106, Appl
37	9	45.0	4	US-09-782-980-107	Sequence 107, Appl
38	9	45.0	4	US-09-737-267-3	Sequence 3, Appl
39	9	45.0	4	US-09-873-676-105	Sequence 104, Appl
40	9	45.0	4	US-09-873-676-105	Sequence 105, Appl
41	9	45.0	4	US-09-736-094-28	Sequence 28, Appl
42	9	45.0	4	US-09-923-261-349	Sequence 199, Appl
43	9	45.0	4	US-09-380-323-5	Sequence 5, Appl
44	9	45.0	4	US-09-380-323-7	Sequence 7, Appl
45	9	45.0	4	US-09-982-172-32	Sequence 32, Appl
46	9	45.0	4	US-09-819-136-6	Sequence 6, Appl
47	9	45.0	4	US-09-837-697A-7	Sequence 7, Appl
48	9	45.0	4	US-09-947-387-3	Sequence 3, Appl
49	9	45.0	4	US-09-947-387-8	Sequence 8, Appl
50	9	45.0	4	US-09-947-387-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-729-873-16
Sequence 16, Application US/09729873
Patent No. US001003621A1
GENERAL INFORMATION:
APPLICANT: Sany Ashkar
TITLE OF INVENTION: Oestrogen In-Derived Characteristic and Identity Agents
TITLE OF INVENTION: and Uses Therefor
FILE REFERENCE: OMZ-123CP
CURRENT APPLICATION NUMBER: US/09/729,873
CURRENT FILING DATE: 2000-12-05
PRIOR APPLICATION NUMBER: 50/129,764
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: PCT/US00/10344
PRIOR FILING DATE: 2000-04-17
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 4
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-729-873-16

Query Match 100.0% Score 20; DB 10; Length 4;
Post-Local Similarity 100.0%; Pred No 1 6405;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEP 4

Db 1 VLEP 4

RESULT 2

US-09-732-411-15

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; Sequence 15, Application US/09732411
; Patent No. US20020208326A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Adhesion Modulatory Peptides and Methods for Use
; FILE REFERENCE: CM2 124CP
; CURRENT APPLICATION NUMBER: US/09/732,411
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/129,709
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: FT/US00/10323
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-732-411-15

Query Match 100.0%; Score 20; DB 10; Length 4;
Best Local Similarity 100.0%; Pred. No 1.6e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 1 VLEP 4

RESULT 3
US-09-732-873-24
; Sequence 24, Application US/09729873
; Patent No. US20020208326A1
; GENERAL INFORMATION:
; APPLICANT: Samy Ashkar
; TITLE OF INVENTION: Caspentin Derived Chemotactic and Inhibitory Agents
; FILE REFERENCE: CM2-123CP
; CURRENT APPLICATION NUMBER: US/09/729,873
; PRIOR FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/123,764
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: FT/US00/10344
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MLD PES
; LOCATION: 11
; OTHER INFORMATION: ACETYLATION
US-09-729-873-24

Query Match 70.0%; Score 14; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No 1.6e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEP 4
Db 1 MLDP 4

RESULT 4
US-09-947-387-23
; Sequence 23, Application US/09947387

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; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Yeana, John P.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han Zhong
; TITLE OF INVENTION: DC US20020150885A1 Fluorogenic or Fluorescent Reporter Molecules
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735 0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-23

Query Match 70.0%; Score 14; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No 1.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4
Db 1 LEP 3

RESULT 5
US-09-947-387-27
; Sequence 27, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Yeana, John P.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han Zhong
; TITLE OF INVENTION: DC US20020150885A1 Fluorogenic or Fluorescent Reporter Molecules
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735 0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-27

```

Query Match 65.0%; Score 13; DB 10; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DEP 4
 :||
 Db 1 VEP 3

RESULT 6
 US-10-087-905-8
 ; Sequence 8, Application US/10087905
 ; Publication No. US20030022152A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Haaland, Perry D.
 ; APPLICANT: Sherman, Douglas B.
 ; APPLICANT: Stewart II, Walter W.
 ; APPLICANT: Lloyd, Sheila A.
 ; APPLICANT: Campbell, Robert L.
 ; TITLE OF INVENTION: METHODS, APPARATUS AND COMPUTER PROGRAMS FOR
 ; FILE REFERENCE: P3250
 ; CURRENT APPLICATION NUMBER: US/10/087,905
 ; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US/09/359,260
 ; PRIOR FILING DATE: 1999-07-22
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: hypothetical
 ; OTHER INFORMATION: peptide
 US 10-087-905-8

Query Match 60.0%; Score 12; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
 :||
 Db 3 EP 4

RESULT 7
 US-09-947-387-13
 ; Sequence 13, Application US/09947387
 ; Patent No. US2002015084A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keana, John F.W.
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han Zhong
 ; TITLE OF INVENTION: NO. US2002015084A1 Fluorogenic or Fluorescent Reporter Molecule
 ; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1736.0290005
 ; CURRENT APPLICATION NUMBER: US/09/947,387
 ; CURRENT FILING DATE: 2001-09-07
 ; PRIOR APPLICATION NUMBER: US 60/061,582
 ; PRIOR FILING DATE: 1997-10-10
 ; PRIOR APPLICATION NUMBER: US 60/145,746
 ; PRIOR FILING DATE: 1998-03-03
 ; PRIOR APPLICATION NUMBER: US-09/168,888
 ; PRIOR FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: Patent In Ver 2.0
 ; SEQ ID NO 13

LENGTH: 4
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Peptide
 US-09-947-387-13

Query Match 60.0%; Score 12; DB 10; Length 4;
 Best Local Similarity 100.0%; Pred. No. 1.6e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
 :||
 Db 2 EP 3

RESULT 8
 US-09-861-097-16
 ; Sequence 16, Application US/09861097
 ; Publication No. US20020102218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KARIN, MICHAEL
 ; APPLICANT: DAVIS, ROGER
 ; APPLICANT: MASAHITO, HIRI
 ; APPLICANT: ANNING, LIN
 ; APPLICANT: DERJARD, BENOIT
 ; TITLE OF INVENTION: ONCOGENEIN PROTEIN KINASE
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FISH & RICHARDSON P.C.
 ; STREET: 4225 Executive Square, Suite 1400
 ; CITY: La Jolla
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92037
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/861,097
 ; FILING DATE: 18-May-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/229,602
 ; FILING DATE: 25-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Haile, Ph.D., Lisa A.,
 ; REGISTRATION NUMBER: 38,347
 ; REFERENCE/SEQ ID NO: 16;
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 678-5070
 ; TELEFAX: (619) 678-5099
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: 1..4
 ; OTHER INFORMATION: /note "Fish & Richardson, ASP - ASP
 ; or Glu"

US-09-861-097-16
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 ; Query Match 55.0%; Score 11; DB 9; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.6e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 2 LEP 4
DB 1 LEP 3

RESULT 9
US-09-031-629A-3
; Sequence 3, Application US/09031629A
; Patent No. US2002015541A1
; GENERAL INFORMATION:
; APPLICANT: Hayashi
; TITLE OF INVENTION: Methods for Treating and Diagnosing Autoimmune Disease
; FILE REFERENCE: MUR/Reisman 17639/1050
; CURRENT APPLICATION NUMBER: US/09/031,629A
; CURRENT FILING DATE: 1998 02 21
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fluorogenic
; OTHER INFORMATION: Peptide used for degradation assays
; NAME/KEY: SITE
; LOCATION: 131
; OTHER INFORMATION: Beta Lactamamide is attached to the C-terminal
; OTHER INFORMATION: Glu
; NAME/KEY: SITE
; LOCATION: 131
; OTHER INFORMATION: The N-terminal Lys contains a carbonyl group
; OTHER INFORMATION: modification
US-09-031-629A-3
Query Match 50.0%; Score 10; DB 10; Length 2
Best Local Similarity 66.7%; Pred No 1.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 LLE 3

RESULT 10
US-08-484-409-25
; Sequence 25, Application US/08484409
; Patent No. US2003007612A1
; GENERAL INFORMATION:
; APPLICANT: Steinman, Lawrence
; APPLICANT: Zamvil, Scott
; TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 201 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104 7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.0
; CURRENT AFFILIATION DATA:
; APPLICATION NUMBER: US/08/484,409
; FILING DATE: 07 JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Markl, David J.
; REGISTRATION NUMBER: 31,392

QY 2 LEP 4
DB 1 LEP 3

RESULT 11
US-09-742-096-26
; Sequence 26, Application US/09742096
; Patent No. US2002015541A1
; GENERAL INFORMATION:
; APPLICANT: DPHULHE, PIERRE
; APPLICANT: DAVPERSIES, PIERRE
; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES
; FILE REFERENCE: 200773050DIV
; CURRENT APPLICATION NUMBER: US/09/742,096
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 08/973,642
; PRIOR FILING DATE: 1998-02-06
; PRIOR APPLICATION NUMBER: PCT/EP96/00894
; PRIOR FILING DATE: 1996-06-12
; PRIOR APPLICATION NUMBER: PP 95/07007
; PRIOR FILING DATE: 1995-06-13
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 26
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-742-096-26
Query Match 50.0%; Score 10; DB 9; Length 4;
Best Local Similarity 66.7%; Pred No 1.6e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 1 VLE 3

RESULT 12
US-10-029-191-16
; Sequence 16, Application US/10029101
; Patent No. US20020160453A1
; GENERAL INFORMATION:
; APPLICANT: CURTIS, ROY A.J.
; TITLE OF INVENTION: NEWFL GENE ENCODING A SODIUM CHANNEL BETA-3 SUBUNIT
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 210147, 00XX/5U1
; CURRENT APPLICATION NUMBER: US/10/029,191
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 09/560,978
; PRIOR FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: US 06/134,198
; PRIOR FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 23
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? LENGTH: 3
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
US-09-312 762A 12

Query Match
Best Local Similarity 45.0%; Score 9; DB 9; Length 4;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EP 4
DB 1 DP 2

RESULT 21
US-08-484-409-13
? Sequence 13, Application US/08484409
? Patent No. US20020607412A1
? GENERAL INFORMATION:
? APPLICANT: Steinman, Lawrence
? APPLICANT: Zamvil, Scott
? TITLE OF INVENTION: METHODS FOR MODULATING THE IMMUNE SYSTEM
? NUMBER OF SEQUENCES: 52
? CORRESPONDENT ADDRESS:
? ADDRESSER: SEED AND BERRY LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: USA
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-WINDOWS
? SOFTWARE: Patent in Release #1 0. Version #1 30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/484,409
? FILING DATE: 07-JUN-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Maki, David J.
? REGISTRATION NUMBER: 31,392
? REFERENCE/PROCT NUMBER: 6000044001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 622-4900
? TELEFAX: (206) 682-6031
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
US-08-484-409-13

Query Match
Best Local Similarity 45.0%; Score 9; DB 8; Length 4;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLE 3
DB 2 ILD 4

RESULT 22
US-09-964-114-5
? Sequence 5, Application US/09964114
? Patent No. US20020156094A1
? GENERAL INFORMATION:
? APPLICANT: Albrecht, Hans P. et al.
? TITLE OF INVENTION: Sulfonamide Interleukin-1Beta Converting Enzyme
? INHIBITORS
? FILE REFERENCE: 22253-68736
```

```
? CURRENT APPLICATION NUMBER: US/09/964,114
? CURRENT FILING DATE: 2001-09-25
? PRIOR APPLICATION NUMBER: 09/284,423
? PRIOR FILING DATE: 1999-04-02
? PRIOR APPLICATION NUMBER: PCT/US97/18196
? PRIOR FILING DATE: 1999-10-09
? PRIOR APPLICATION NUMBER: 60/028,313
? PRIOR FILING DATE: 1996-10-11
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 5
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? NAME/KEY: UNSURE
? LOCATION: (1)...(4)
? OTHER INFORMATION: Acetyl group attached to 5' end and 11MA group
? OTHER INFORMATION: attached to 3' end
? OTHER INFORMATION: Description of Artificial Sequence: Chemically
? OTHER INFORMATION: synthesized
US-09-964-114-5

Query Match
Best Local Similarity 45.0%; Score 9; DB 9; Length 4;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LE 3
DB 1 LE 2

RESULT 23
US-09-900-936-7
? Sequence 7, Application US/09900936
? Patent No. US20020165141A1
? GENERAL INFORMATION:
? APPLICANT: Rodgers, Kathleen
? APPLICANT: Dizerega, Gere
? TITLE OF INVENTION: Methods for Promoting Conditional Cell Proliferation
? TITLE OF INVENTION: or Differentiation
? FILE REFERENCE: 00-506-A
? CURRENT APPLICATION NUMBER: US/99/900,936
? CURRENT FILING DATE: 2001-07-09
? NUMBER OF SEQ ID NOS: 50
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO 7
? LENGTH: 4
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: A1 (5-B)
US-09-900-936-7

Query Match
Best Local Similarity 45.0%; Score 9; DB 9; Length 4;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LEP 4
DB 1 IHP 3

RESULT 24
US-10-085-801A-1
? Sequence 1, Application US/10085801A
? Patent No. US20020169123A1
? GENERAL INFORMATION:
? APPLICANT: El-Deiry, Wafik S.
? APPLICANT: Kim, Kunhong
? TITLE OF INVENTION: Regulating Apoptosis in TRAIL-Resistant Cancer Cells
? WHILE PROMOTING NO. US/02/015,609A1, NO. US/02/015,609A1
? FILE REFERENCE: 22253-68736
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; CURRENT APPLICATION NUMBER: US/10/085,801A
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: 60/271,674
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: commercially
; OTHER INFORMATION: available
US-10-085-801A-1

```

```

Query Match      45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 100.0%; Pred No 1 6e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      2 LE 3
        ||
Db       1 LE 2

```

```

RESULT 25
US-10-101-487-101
; Sequence 101, Application US/10101487
; Patent No.: US20030169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFOUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K
; APPLICANT: WAGGNER JR., DAVID W
; TITLE OF INVENTION: RESONANT PREDECTION OF POLYANIONIC POLYMERS AND USES
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10/101,487
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-101-487-101

```

```

Query Match      45.0%; Score 9; DB 9; Length 4;
Best Local Similarity 50.0%; Pred No 1 6e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      3 EP 4
        :|
Db       2 QP 3

```

```

Search completed: March 6, 2003, 09:49:32
Job time : 35 secs

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GenCore version 5.1.3
Copyright (c) 1991 - 2003 CompuGen Ltd

OM protein - protein search, using sw mode!

Run on: March 5, 2003, 09:37:56, Search time 29 Seconds
(without alignments)
4.05a Millib. will updates/sec

Title: US-09-732 411 15

Perfect score: 26

Sequence: 1 VLEP 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Seatched: 262174 seqs, 2342322 residues

Total number of hits satisfying chosen parameters: 9158

Minimum DB seq length: 0

Maximum DB seq length: 4

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database: Issued Patents AA.*

- 1: /cgm2_6/prodata/1/iaa/5A.COMB.pep.*
- 2: /cgm2_6/prodata/1/iaa/5B.COMB.pep.*
- 3: /cgm2_6/prodata/1/iaa/6A.COMB.pep.*
- 4: /cgm2_6/prodata/1/iaa/6B.COMB.pep.*
- 5: /cgm2_6/prodata/1/iaa/6C.COMB.pep.*
- 6: /cgm2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	15	75.0	4	1	US-08-240-712-5
2	15	75.0	4	1	US-08-443-890-5
3	15	75.0	4	4	US-08-084-562-5
4	15	75.0	4	5	PCT-US92 00752-5
5	14	70.0	4	1	US-08-336-343A-38
6	14	70.0	4	2	US-08-609-271-1
7	14	70.0	4	4	US-08-188-374-1
8	14	70.0	4	4	US-09-130-193-16
9	14	70.0	4	4	US-09-357-952-23
10	14	70.0	4	4	US-08-521-560-23
11	14	70.0	4	4	US-08-168-888-23
12	14	70.0	4	4	US-09-513-783A-100
13	13	65.0	4	2	US-08-441-871-28
14	13	65.0	4	4	US-09-330-970-16
15	13	65.0	4	4	US-09-330-970-14
16	13	65.0	4	4	US-08-859-247-31
17	13	65.0	4	4	US-09-357-952-27
18	13	65.0	4	4	US-08-521-560-27
19	13	65.0	4	4	US-08-168-888-27
20	13	65.0	4	4	US-09-187-859-199
21	12	60.0	4	1	US-07-714-167E-8
22	12	60.0	4	1	US-07-714-167E-11
23	12	60.0	4	1	US-07-729-153-7
24	12	60.0	4	1	US-08-122-546-1
25	12	60.0	4	1	US-08-280-443-39
26	12	60.0	4	1	US-08-457-459-39
27	12	60.0	4	1	US-08-224-968-5

28	12	60.0	4	1	US-08-555-678-39
29	12	60.0	4	1	US-08-477-509B-7
30	12	60.0	4	1	US-08-477-509B-31
31	12	60.0	4	2	US-08-609-271-2
32	12	60.0	4	2	US-08-609-271-3
33	12	60.0	4	2	US-08-609-271-4
34	12	60.0	4	2	US-08-609-271-5
35	12	60.0	4	2	US-08-764-938-1
36	12	60.0	4	3	US-08-482-085B-7
37	12	60.0	4	3	US-08-482-085B-31
38	12	60.0	4	3	US-08-415-655-3
39	12	60.0	4	3	US-08-624-405-7
40	12	60.0	4	3	US-08-105-678A-52
41	12	60.0	4	3	US-09-131-052-1
42	12	60.0	4	4	US-08-188-374-2
43	12	60.0	4	4	US-08-188-374-3
44	12	60.0	4	4	US-08-188-374-4
45	12	60.0	4	4	US-08-188-374-5
46	12	60.0	4	4	US-08-891-271-10
47	12	60.0	4	4	US-04-131-053A-1
48	12	60.0	4	4	US-09-035-859-47
49	12	60.0	4	4	US-08-457-952-13
50	12	60.0	4	4	US-09-421-209-50

ALIGNMENTS

RESULT 1
US-08-240-712-5
; Sequence 5, Application US/09240712
; Patent No. 5599907
; GENPAT INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: WATHEWS, ANTHONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,712
; FILING DATE: 09-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/09752
; FILING DATE: 13-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, IVER P
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANDERSON-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 628-5197
; TELEFAX: 202-737-3508
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-240-712-5

Query Match 75.0%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1 9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSP 4
|||
Db 1 VLSP 4

RESULT 2

US-08-443-890-5
; Sequence 5, Application US/08413896
; Patent No. 5739011
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATTHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pat-in Release #1.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,890
FILING DATE: 31-MAY-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/240,712
FILING DATE: 09-MAY-1994
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 13-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/PACKET NUMBER: ANDERSON-6-PCT
TELEPHONE: 202-629-5197
TELEFAX: 202-717-3528
TELEX: 249633
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-443-890-5

Query Match 75.0%; Score 15; DB 1; Length 4;
Best Local Similarity 75.0%; Pred. No. 1 9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSP 4
|||
Db 1 VLSP 4

RESULT 3

US-09-058-562-5
; Sequence 5, Application US/09058562A
; Patent No. 6194256

GENERAL INFORMATION:

APPLICANT: Anderson, David C.
APPLICANT: Matthews, Antony James
APPLICANT: Stetler, Gary L.
TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC HEMOGLOBINS
FILE REFERENCE: PXR 2087
CURRENT APPLICATION NUMBER: US/09/058,562A
CURRENT FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 08/240,712
PRIOR FILING DATE: 1994-05-09
PRIOR APPLICATION NUMBER: PCT/US92/09752
PRIOR FILING DATE: 1993-05-13
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5
LENGTH: 4
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION Description of Artificial Sequence: Peptide
US-09-058-562-5

Query Match 75.0%; Score 15; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 1 9e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLSP 4
|||
Db 1 VLSP 4

RESULT 4

PCT-US92-09752-5
; Sequence 5, Application PCT/US9209752
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DAVID C.
; APPLICANT: MATTHEWS, ANTONY JAMES
; APPLICANT: STETLER, GARY L.
; TITLE OF INVENTION: PRODUCTION AND USE OF MULTIMERIC
; TITLE OF INVENTION: HEMOGLOBINS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/09752
FILING DATE: 1993-05-13
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P
REGISTRATION NUMBER: 28,005
REFERENCE/PACKET NUMBER: ANDERSON-6-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-629-5197
TELEFAX: 202-717-3528
TELEX: 249633
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US92-09752-5

```

Query Match      75.0%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches      3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 VLEP 4
|||
db 1 VLSP 4

RESULT 5
 US-OR-346-443A-18
 ; Sequence 18, Application US/0836343A
 ; Patent No. 5677144
 ; GENERAL INFORMATION
 ; APPLICANT: Ullrich, Axel
 ; APPLICANT: Alves, Frank
 ; TITLE OF INVENTION: ccr 2, A NOVEL TYROSINE KINASE

Query Match	70.0%	Score 14	DB 1	Length 4
Best Local Similarity	66.7%	Pred. No. 1.9e+05		
Matches	2	Mismatch 0	Inkels	0
				525

2 LEP 4
: ||
2 MEP 4

```

RESULT 6
; US 08-609-271-1
; Sequence 1, Application US/08609271
; Patent No. 5811264
; GENERAL INFORMATION:
; APPLICANT: Aitken, Jacqueline F.
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Somatogen, Inc.

```

STREET: 2545 Central Avenue, Site PD-1
CITY: Boulder
STATE: Colorado
ZIP: 80301

Query Match 70.0%; Score 14; DB 2; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.9e+05;
Matches 2; Conservative 2; Mismatches 0; Indels

Qy	1	VLEP	4
	:	:	:
pb	1	MLOP	4

```

RESULT 7
US-08-188-374-1
; Sequence 1, Application US/08188374B
; Patent No. 6140071
; GENERAL INFORMATION:
; APPLICANT: Aitken F., Jacqueline
; APPLICANT: Apostol, Izydor Z.
; APPLICANT: Lippincott, Julie A.
; APPLICANT: Levine, Joseph D.
; TITLE OF INVENTION: Proteins with Mutations to Decrease N-Terminal Methylation
; FILE REFERENCE: BXTB 1953
; CURRENT APPLICATION NUMBER: US/08/188,374B
; CURRENT FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: METHYLATION-- N terminal Met
US-08-188-174-1

```

Query Match 70.0%, Score 14, DB 4, Length 4;
Best Local Similarity 50.0%, Pred. No. 1.9e+05;
Matches 2, Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 VLEP 4
|||
DB 1 MLEP 4

RESULT 8

US-09-130-193-16
; Sequence 16, Application US/09130193
; Patent No. 6235493
; GENERAL INFORMATION:
; APPLICANT: EUGENE R. BISSELL ET AL
; TITLE OF INVENTION: AMINO ACID SUBSTITUTED-
; CRESYL VIOLET, SYNTHETIC
; TITLE OF INVENTION: FLUORESCENT SUBSTRATES
; TITLE OF INVENTION: FOR THE ANALYSIS OF
; TITLE OF INVENTION: AGENTS IN INDIVIDUAL IN
; TITLE OF INVENTION: VIVO CELLS OR TISSUE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PETERS, VERNY, JONES & BIK A, LLP
; STREET: 385 Sherman Avenue, Suite 6
; CITY: Palo Alto
; STATE: California
; COUNTRY: United States of America
; ZIP: 94306-1840
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Kb storage
; COMPUTER: PC
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/130,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/026,062
; FILING DATE: SEPTEMBER 23, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HOWARD P. PETERS
; REGISTRATION NUMBER: 29,202
; REFERENCE TO PCT NUMBER: 3594 11-17(ME)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 324-1677 X 20
; TELEFAX: (650) 324-1678
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-130-193-16

Query Match 70.0%, Score 14, DB 4, Length 4;
Best Local Similarity 66.7%, Pred. No. 1.9e+05;
Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4
|||
DB 1 IEP 3

RESULT 9

US-09-357-952-23
; Sequence 23, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong

; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-Cell
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735 0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US 09 357-952-23

Query Match 70.0%, Score 14, DB 4, Length 4;
Best Local Similarity 66.7%, Pred. No. 1.9e+05;
Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4
|||
DB 1 IEP 3

RESULT 10

US-09-521-650-23
; Sequence 23, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735 0040002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/169,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,592
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 23
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-23

Query Match 70.0%, Score 14, DB 4, Length 4;
Best Local Similarity 66.7%, Pred. No. 1.9e+05;
Matches 2, Conservative 1, Mismatches 0, Indels 0, Gaps 0;

QY 2 LEP 4
|||
DB 1 IEP 3

RESULT 11

US-09-168-888-23
 ; Sequence 23, Application US/0916888
 ; Patent No. 6342611
 ; GENERAL INFORMATION:
 ; APPLICANT: Weber, Eckard
 ; APPLICANT: Cai, Sui Xiong
 ; APPLICANT: Keane, John F W
 ; APPLICANT: Drewe, John A.
 ; APPLICANT: Zhang, Han-Zhong
 ; TITLE OF INVENTION: No. 6342611 Fluorogenic or Fluorescent Reporter Molecules and
 ; TITLE OF INVENTION: Their Applications for Whole Cell Fluorescence
 ; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
 ; TITLE OF INVENTION: Use Thereof
 ; FILE REFERENCE: 1735.0290002
 ; CURRENT APPLICATION NUMBER: US/09/168,888
 ; CURRENT FILING DATE: 1998-10-09
 ; EARLIER APPLICATION NUMBER: US 60/061,582
 ; EARLIER FILING DATE: 1997-10-10
 ; EARLIER APPLICATION NUMBER: US 09/033,661
 ; EARLIER FILING DATE: 1998-03-03
 ; NUMBER OF SEQ ID NOS: 142
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 23
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
 ; OTHER INFORMATION: Peptide

US-09-168-888-23

Query Match 70.0%, Score 14, DB 4, Length 4,
 Best Local Similarity 66.7%, Pred No 1,90,05,
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 1 LEP 3

RESULT 12

US-09-513-783A-100
 ; Sequence 100, Application US/09513783A
 ; Patent No. 6416959
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97 022,11
 ; CURRENT APPLICATION NUMBER: US/09/513,783A
 ; CURRENT FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 100
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Granzyme B
 ; OTHER INFORMATION: substrate recognition sequence

US-09-513-783A-100

Query Match 70.0%, Score 14, DB 4, Length 4,
 Best Local Similarity 66.7%, Pred No 1,90,05,
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 1 LEP 3

RESULT 13

US-08-441-871-28
 ; Sequence 28, Application US/08441871
 ; Patent No. 5846765
 ; GENERAL INFORMATION:
 ; APPLICANT: Matthews, David J.
 ; APPLICANT: Wells, James A.
 ; APPLICANT: Zoller, Mark J.
 ; TITLE OF INVENTION: Identification of No. 5846765-el Substrates
 ; NUMBER OF SEQUENCES: 152
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25 inch, 360 KB floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: patin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/441,871
 ; FILING DATE: 16-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/418928
 ; FILING DATE: 05-APR-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/161692
 ; FILING DATE: 03-DEC-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/864452
 ; FILING DATE: 06-APR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/09133
 ; FILING DATE: 03-DEC-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/743614
 ; FILING DATE: 09-AUG-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/715300
 ; FILING DATE: 14-JUN-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/683400
 ; FILING DATE: 10-APR-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/621667
 ; FILING DATE: 03-DEC-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Daryl B.
 ; REGISTRATION NUMBER: 32,637
 ; REFERENCE/DOC#ET NUMBER: 645907201
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225 1249
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 4 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear

US-08-441-871-28

Query Match 65.0%, Score 13, DB 2, Length 4;
 Best Local Similarity 66.7%, Pred No 1,90,05,
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LEP 4

DB 2 LDP 4

```

RESULT 14
US-09-330-970-16
; Sequence 34, Application US/09330970
; Patent No. 6145876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A Nucleoside Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-16

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
   |||
Db 2 VLE 4

```

```

RESULT 15
US-09-330-970-34
; Sequence 34, Application US/09330970
; Patent No. 6145876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: White, David
; TITLE OF INVENTION: A Nucleoside Cyclic Nucleotide
; TITLE OF INVENTION: Phosphodiesterase
; FILE REFERENCE: 5800-28
; CURRENT APPLICATION NUMBER: US/09/330,970
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-330-970-34

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
   |||
Db 2 VLE 4

```

```

RESULT 16
US-09-859-242-31
; Sequence 31, Application US/08859242
; Patent No. 6159938
; GENERAL INFORMATION:
; APPLICANT: Sartech, Inc
; APPLICANT: Albert C. Gyorkos
; APPLICANT: Lyle W. Spruce

```

```

; APPLICANT: Axel H. Leimer
; APPLICANT: John C. Cheronis
; TITLE OF INVENTION: Serine Protease Inhibitors Comprising
; TITLE OF INVENTION: Alpha-Peto Heterocycles
; FILE REFERENCE: 361210 006 (21 CIP)
; CURRENT APPLICATION NUMBER: US/09/859,242C
; CURRENT FILING DATE: 1997-05-20
; EARLIER APPLICATION NUMBER: US 08/345,820
; EARLIER FILING DATE: 1996-11-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Serine Protease
US-09-859-242-31

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 100.0%; Pred No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 VLE 3
   |||
Db 1 VLE 3

```

```

RESULT 17
US-09-357-952-27
; Sequence 27, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-Cell
; TITLE OF INVENTION: Fluorescence Screening Assays for Cusapases, Peptidases, Proteases
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 08/093,642
; EARLIER FILING DATE: 91-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent In Ver 2.0
; SEQ ID NO 27
; LENGTH: 4
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-27

```

```

Query Match 65.0%; Score 13; DB 4; Length 4;
Best Local Similarity 66.7%; Pred No. 1.9e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 2 LEP 4
   |||
Db 1 VEP 3

```

```

RESULT 18
US-09-521-650-27
; Sequence 27, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han Zhong

```